

WEST Search History

Hide Items Restore Clear Cancel

DATE: Friday, December 19, 2003

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L9	L8 and I5	3
<input type="checkbox"/>	L8	L7 and (dna or cdna or nucleotide or polynucleotide or nucleic acid)	4
<input type="checkbox"/>	L7	L6 and (prunus serotina)	7
<input type="checkbox"/>	L6	Hydroxynitrile lyase or Acetone cyanohydrin lyase or Hydroxymandelonitrile lyase or S Hydroxynitrilase or S Hydroxynitrile lyase or S Oxynitrilase or Mandelonitrile lyase or R Oxynitrilase	80
<input type="checkbox"/>	L5	L4 or I3 or I2 or I1	25233
<input type="checkbox"/>	L4	(536/23.2)!..ccls.	9972
<input type="checkbox"/>	L3	(435/320.1)!..ccls.	21758
<input type="checkbox"/>	L2	(435/232)!..ccls.	427
<input type="checkbox"/>	L1	(435/183)!..ccls.	4282

END OF SEARCH HISTORY

Hit List

[Clear](#)[Generate Collection](#)[Print](#)[Fwd Refs](#)[Bkwd Refs](#)[Generate OACS](#)

Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 20030148440 A1

L7: Entry 1 of 7

File: PGPB

Aug 7, 2003

PGPUB-DOCUMENT-NUMBER: 20030148440

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030148440 A1

TITLE: Process for producing hydroxynitrile lyases

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	-----------	-------

☐ 2. Document ID: US 20030129714 A1

L7: Entry 2 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129714

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129714 A1

TITLE: Process for preparing protected, enantiomer-enriched cyanohydrins by in-situ derivatization

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	-----------	-------

☐ 3. Document ID: US 20030129713 A1

L7: Entry 3 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129713

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129713 A1

TITLE: Process for preparing enantiomer-enriched cyanohydrins using acetals or ketals as substrates

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	-----------	-------

☐ 4. Document ID: US 20030129712 A1

L7: Entry 4 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129712

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129712 A1

TITLE: Process for preparing heterocyclic (R)- and (S)-cyanohydrins

☐ 5. Document ID: US 20030119099 A1

L7: Entry 5 of 7

File: PGPB

Jun 26, 2003

PGPUB-DOCUMENT-NUMBER: 20030119099

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030119099 A1

TITLE: Genes containing a DNA sequence coding for hydroxynitrile lyase, recombinant proteins derived therefrom and having hydroxynitrile lyase activity, and use thereof

☐ 6. Document ID: US 20010051335 A1

L7: Entry 6 of 7

File: PGPB

Dec 13, 2001

PGPUB-DOCUMENT-NUMBER: 20010051335

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

☐ 7. Document ID: US 6096545 A

L7: Entry 7 of 7

File: USPT

Aug 1, 2000

US-PAT-NO: 6096545

DOCUMENT-IDENTIFIER: US 6096545 A

**** See image for Certificate of Correction ****

TITLE: Phosphate starvation-inducible proteins

Clear

Generate Collection

Print

Fwd Refs

Bkwd Refs

Generate OACS

Terms

Documents

L6 and (prunus serotina)

7

Display Format:

Change Format

[Previous Page](#)

[Next Page](#)

[Go to Doc#](#)

=> s hydroxynitrile lyase/cn
L1 3 HYDROXYNITRILE LYASE/CN

=> d 1-3

L1 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 112567-89-2 REGISTRY
CN Lyase, acetone-cyanohydrin (9CI) (CA INDEX NAME)
OTHER NAMES:
CN (S)-Hydroxynitrile lyase
CN .alpha.-Hydroxynitrile lyase
CN Acetone-cyanohydrin lyase
CN E.C. 4.1.2.37
CN E.C. 4.1.2.39
CN Hydroxynitrile lyase
MF Unspecified
CI MAN
SR CA
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT, CIN,
TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

67 REFERENCES IN FILE CA (1907 TO DATE)
7 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
67 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9075-38-1 REGISTRY
CN Lyase, hydroxymandelonitrile (9CI) (CA INDEX NAME)
OTHER NAMES:
CN (S)-p-Hydroxymandelonitrile lyase
CN E.C. 4.1.2.11
CN Hydroxynitrile lyase
CN S-Hydroxynitrilase
CN S-Hydroxynitrile lyase
CN S-Oxynitrilase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT, CEN,
CHEMINFORMRX, CIN, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

73 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
74 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9024-43-5 REGISTRY
CN Lyase, mandelonitrile (9CI) (CA INDEX NAME)
OTHER NAMES:
CN E.C. 4.1.2.10
CN Hydroxynitrile lyase
CN Mandelonitrile lyase
CN R-Hydroxynitrile lyase
CN R-Oxynitrilase
CN R-Oxynitrilase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT,
CHEMCATS, CHEMINFORMRX, CHEMLIST, CSCHEM, IFICDB, IFIPAT, IFIUDB,
TOXCENTER, USPAT2, USPATFULL
Other Sources: EINECS**
(*Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

210 REFERENCES IN FILE CA (1907 TO DATE)
4 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
212 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d full his

(FILE 'HOME' ENTERED AT 13:24:28 ON 18 DEC 2003)

FILE 'REGISTRY' ENTERED AT 13:24:33 ON 18 DEC 2003

L1 3 SEA ABB=ON PLU=ON HYDROKYNITRILE LYASE/CN
D 1-3

FILE 'HCAPLUS' ENTERED AT 13:25:00 ON 18 DEC 2003

E PRUNUS SEROTINA/CT

E E3+ALL

FILE 'REGISTRY' ENTERED AT 13:25:42 ON 18 DEC 2003

SET SMARTSELECT ON

L2 SEL PLU=ON L1 1- CHEM : 18 TERMS

SET SMARTSELECT OFF

FILE 'HCAPLUS' ENTERED AT 13:25:42 ON 18 DEC 2003

L3 378 SEA ABB=ON PLU=ON L2

L4 17 SEA ABB=ON PLU=ON L3 (L) (PRUNUS SEROTINA)

L5 16 SEA ABB=ON PLU=ON L4 AND PD<20010116

L6 6 SEA ABB=ON PLU=ON L5 AND (DNA OR CDNA OR NUCLEOTIDE OR
POLYNUCLEOTIDE OR NUCLEIC ACID)

=> d ibib ab 1-6

L6 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:258627 HCAPLUS

DOCUMENT NUMBER: 131:98302

TITLE: Molecular analysis of (R)-(+)-mandelonitrile lyase microheterogeneity in black cherry

AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.

CORPORATE SOURCE: Department of Biological Sciences, The University of Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1999), 119(4), 1535-1546

CODEN: PLPHAY; ISSN: 0032-0889

PUBLISHER: American Society of Plant Physiologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10), which plays a key role in cyanogenesis in rosaceous stone fruits, occurs in black cherry (*Prunus serotina* Ehrh.) homogenates as several closely related isoforms. Biochem. and mol. biol. methods were used to investigate MDL microheterogeneity and function in this species. Three novel MDL cDNAs of high sequence identity (designated MDL2, MDL4, and MDL5) were isolated. Like MDL1 and MDL3 cDNAs (Z. Hu, J.E. Poulton [1997] Plant Physiol 115: 1359-1369), they had open reading frames that predicted a FAD-binding site, multiple N-glycosylation sites, and an N-terminal signal sequence. The N terminus of an MDL isoform purified from seedlings matched the derived amino acid sequence of the MDL4 cDNA. Genomic sequences corresponding to the MDL1, MDL2, and MDL4 cDNAs were obtained by polymerase chain reaction amplification of genomic DNA. Like the previously reported md13 gene, these genes are interrupted at identical positions by three short, conserved introns. Given their overall similarity, we conclude that the genes md11, md12, md13, md14, and md15 are derived from a common ancestral gene and constitute members of a gene family. Genomic Southern-blot anal. showed that this family has approx. eight members. Northern-blot anal. using gene-specific probes revealed differential expression of the genes md11, md12, md13, md14, and md15.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:583095 HCAPLUS

DOCUMENT NUMBER: 129:299647

TITLE: Molecular cloning of the cDNA coding for the (R)-(+)-mandelonitrile lyase of *Prunus amygdalus*. Temporal and spatial expression patterns in flowers and mature seeds

AUTHOR(S): Suelves, Monica; Puigdomenech, Pere

CORPORATE SOURCE: Dep. Genetica Molecular, CID-CSIC, Barcelona, E-08034, Spain

SOURCE: Planta (1998), 206(3), 388-393

CODEN: PLANAB; ISSN: 0032-0935

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A gene highly expressed in the floral organs of almond (*Prunus amygdalus*) and coding for the cyanogenic enzyme (R)-(+)-mandelonitrile lyase (EC 4.1.2.10), has been identified and the full-length cDNA sequenced. The temporal expression pattern in maturing seeds and during floral development was analyzed by RNA blot, and the highest mRNA levels were detected in floral tissues. The spatial mRNA accumulation pattern in almond flower buds was also analyzed by in-situ hybridization. The mRNA levels were compared during seed maturation and floral development in fruit and floral samples from cultivars classified as homozygous or heterozygous for the sweet-almond trait or homozygous for the bitter trait. No correlation was found between these characteristics and levels of mandelonitrile lyase mRNA, suggesting that the presence of this protein is not the limiting factor in the prodn. of hydrogen cyanide.

L6 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:804853 HCAPLUS
 DOCUMENT NUMBER: 128:137053
 TITLE: Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene
 AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
 CORPORATE SOURCE: Department of Biological Sciences, The University of Iowa, Iowa City, IA, 52242, USA
 SOURCE: Plant Physiology (1997), 115(4), 1359-1369
 CODEN: PLPHAY; ISSN: 0032-0889
 PUBLISHER: American Society of Plant Physiologists
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10) plays a key role in cyanogenesis in rosaceous stone fruits. An MDL gene (mdl3) and its corresponding cDNA (MDL3) were isolated from black cherry (*Prunus serotina*) and characterized. The mdl3 gene contains 2292 bp of the 5' flanking region, the entire coding region, and 300 bp of the 3' flanking region. The coding region is interrupted by three short introns, of which one possesses the unusual GC-AG splice junction dinucleotides. This gene encodes a polypeptide of 573 amino acids that includes a putative signal sequence, 13 potential N-glycosylation sites, and a presumptive FAD-binding site. To determine whether the 5' flanking region of the mdl3 gene is capable of driving MDL expression, it was fused to the β -glucuronidase reporter gene for *Agrobacterium*-mediated transformation into tobacco. Matching endogenous MDL expression patterns, β -glucuronidase staining was observed in maturing embryos and seeds; it also occurred in postembryonic tissues, especially in association with vascular tissues. After developing a homologous transient transformation system to facilitate identification of putative regulatory sequences, we demonstrated that 125 bp (-107 to +18) of the 5' flanking sequence of the mdl3 gene is sufficient for MDL expression in protoplasts derived from immature black cherry embryos.
 REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:142643 HCAPLUS
 DOCUMENT NUMBER: 126:235180
 TITLE: Molecular cloning of acetone cyanohydrin lyase from flax (*Linum usitatissimum*). Definition of a novel class of hydroxynitrile lyases
 AUTHOR(S): Trummer, Klaus; Wajant, Harald
 CORPORATE SOURCE: Institute of Cell Biology and Immunology, University of Stuttgart, Stuttgart, 70569, Germany
 SOURCE: Journal of Biological Chemistry (1997), 272(8), 4770-4774
 CODEN: JBCHA3; ISSN: 0021-9258
 PUBLISHER: American Society for Biochemistry and Molecular Biology
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB Acetone cyanohydrin lyase from *Linum usitatissimum* is a hydroxynitrile lyase (HNL) which is involved in the catabolism of cyanogenic glycosides in young seedlings of flax. The authors have isolated a full-length cDNA clone encoding *L. usitatissimum* HNL (LuHNL) from a cDNA expression library by immunoscreening. LuHNL cDNA was expressed in *Escherichia coli* and isolated from the resp. sol. fraction in an active form which was biochemically indistinguishable from the natural enzyme. An open reading frame of 1266 base pairs encodes for a protein of 45,780 kDa. The derived amino acid sequence shows no overall homologies to the date cloned HNLs, but has significant similarities to members of the alc. dehydrogenase (ADH) family of enzymes. In particular, the cysteine and histidine residues responsible for coordination of an active site Zn²⁺ and a second structurally important Zn²⁺ in alc. dehydrogenases are conserved. Nevertheless, the authors found neither alc. dehydrogenase activity in LuHNL nor HNL activity in ADH. Moreover, well known inhibitors of ADHs, which interfere with the coordination of the active site Zn²⁺, fail to

affect HNL activity of LuHNL, suggesting principally different mechanisms of cyanohydrin cleavage and alc. oxidn. Interestingly, LuHNL like ADH and *Prunus serotina* (PshNL) possesses an ADP-binding .beta..alpha..beta. unit motif, pointing to the possibility that the non-flavoprotein PshNL and the flavoprotein LuHNL have developed from two independent lines of evolution of a common ancestor with an ADP-binding .beta..alpha..beta. unit.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:811505 HCAPLUS

DOCUMENT NUMBER: 123:334898

TITLE: Temporal and spatial expression of amygdalin hydrolase and (R)-(+)-mandelonitrile lyase in black cherry seeds
AUTHOR(S): Zheng, Liansheng; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sciences, Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1995), 109(1), 31-9

CODEN: PLPHAY; ISSN: 0032-0889

PUBLISHER: Dekker

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In black cherry (*Prunus serotina* Ehrh.) macerates, the cyanogenic diglucoside (R)-amygdalin undergoes stepwise degradn. to HCN catalyzed by amygdalin hydrolase (AH), prunasin hydrolase, and (R)-(+)-mandelonitrile lyase (MDL). A near full-length AH cDNA clone (pAH1), whose insert encodes the isoenzyme AH I, has been isolated and sequenced. AH I exhibits several features characteristic of .beta.-glucosidases of the BGA family, including their likely nucleophile center (isoleucine-threonine-glutamic acid-asparagine-glycine) and acid catalyst (asparagine-glutamic acid-proline/isoleucine) motifs. The temporal expression of AH and MDL in ripening fruit was analyzed by northern blotting. Neither mRNA was detectable until approx. 40 days after flowering (DAF), when embryos first became visible to the naked eye. Both mRNAs peaked at approx. 49 DAF before declining to negligible levels when the fruit matured (82 DAF). Taken together with enzyme activity data, these time courses suggest that AH and MDL expression may be under transcriptional control during fruit maturation. In situ hybridization anal. indicated that AH transcripts are restricted to the procambium, whereas MDL transcripts are localized within cotyledonary parenchyma cells. These tissue-specific distributions are consistent with the major locations of AH and MDL protein in mature seeds previously detd. by immunocytochem. (E. Swain, C.P.Li, and J.E. Poulton [1992] Plant Physiol 100:291-300).

L6 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:47094 HCAPLUS

DOCUMENT NUMBER: 120:47094

TITLE: Cloning of cDNA of *Prunus serotina* (R)-(+)-mandelonitrile lyase and identification of a putative FAD-binding site

AUTHOR(S): Cheng, I Ping; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant and Cell Physiology (1993), 34(7),

1139-43

CODEN: PCPHA5; ISSN: 0032-0781

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A full-length cDNA clone encoding the flavoprotein (R)-(+)-mandelonitrile lyase was isolated from a black cherry (*Prunus serotina*) cDNA expression library and sequenced. A putative FAD-binding site was identified near the N-terminus of this enzyme by comparing its deduced amino acid sequence with those of other FAD- and NAD-binding proteins.

=> d 15 ibib ab 1-16

L5 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1999:258627 HCAPLUS
DOCUMENT NUMBER: 131:98302
TITLE: Molecular analysis of (R)-(+)-mandelonitrile lyase
microheterogeneity in black cherry
AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
CORPORATE SOURCE: Department of Biological Sciences, The University of
Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1999), 119(4), 1535-1546
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC
4.1.2.10), which plays a key role in cyanogenesis in rosaceous stone
fruits, occurs in black cherry (*Prunus serotina* Ehrh.)
homogenates as several closely related isoforms. Biochem. and mol. biol.
methods were used to investigate MDL microheterogeneity and function in
this species. Three novel MDL cDNAs of high sequence identity (designated
MDL2, MDL4, and MDL5) were isolated. Like MDL1 and MDL3 cDNAs (Z. Hu,
J.E. Poulton [1997] Plant Physiol 115: 1359-1369), they had open reading
frames that predicted a FAD-binding site, multiple N-glycosylation sites,
and an N-terminal signal sequence. The N terminus of an MDL isoform
purified from seedlings matched the derived amino acid sequence of the
MDL4 cDNA. Genomic sequences corresponding to the MDL1, MDL2, and MDL4
cDNAs were obtained by polymerase chain reaction amplification of genomic
DNA. Like the previously reported md13 gene, these genes are interrupted
at identical positions by three short, conserved introns. Given their
overall similarity, we conclude that the genes md11, md12, md13, md14, and
md15 are derived from a common ancestral gene and constitute members of a
gene family. Genomic Southern-blot anal. showed that this family has
approx. eight members. Northern-blot anal. using gene-specific probes
revealed differential expression of the genes md11, md12, md13, md14, and
md15.
REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1999:230470 HCAPLUS
DOCUMENT NUMBER: 131:28519
TITLE: The mandelonitrile lyase gene
family in *Prunus serotina*
AUTHOR(S): Hu, Zihua
CORPORATE SOURCE: Univ. of Iowa, Iowa City, IA, USA
SOURCE: (1998) 196 pp. Avail.: UMI, Order No.
DA9904300
From: Diss. Abstr. Int., B 1999, 59(9), 4632
DOCUMENT TYPE: Dissertation
LANGUAGE: English
AB Unavailable

L5 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:583095 HCAPLUS
DOCUMENT NUMBER: 129:299647
TITLE: Molecular cloning of the cDNA coding for the
(R)-(+)-mandelonitrile lyase of *Prunus amygdalus*.
Temporal and spatial expression patterns in flowers
and mature seeds
AUTHOR(S): Suelves, Monica; Puigdomenech, Pere
CORPORATE SOURCE: Dep. Genetica Molecular, CID-CSIC, Barcelona, E-08034,
Spain
SOURCE: Planta (1998), 206(3), 388-393
CODEN: PLANAB; ISSN: 0032-0935
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A gene highly expressed in the floral organs of almond (*Prunus amygdalus*)

and coding for the cyanogenic enzyme (R)-(+)-mandelonitrile lyase (EC 4.1.2.10), has been identified and the full-length cDNA sequenced. The temporal expression pattern in maturing seeds and during floral development was analyzed by RNA blot, and the highest mRNA levels were detected in floral tissues. The spatial mRNA accumulation pattern in almond flower buds was also analyzed by in-situ hybridization. The mRNA levels were compared during seed maturation and floral development in fruit and floral samples from cultivars classified as homozygous or heterozygous for the sweet-almond trait or homozygous for the bitter trait. No correlation was found between these characteristics and levels of mandelonitrile lyase mRNA, suggesting that the presence of this protein is not the limiting factor in the prodn. of hydrogen cyanide.

L5 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:804853 HCAPLUS

DOCUMENT NUMBER: 128:137053

TITLE: Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene

AUTHOR(S): Hu, Zihua; Poulton, Jonathan B.

CORPORATE SOURCE: Department of Biological Sciences, The University of Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1997), 115(4), 1359-1369

CODEN: PLPHAY; ISSN: 0032-0889

PUBLISHER: American Society of Plant Physiologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10) plays a key role in cyanogenesis in rosaceous stone fruits. An MDL gene (mdl3) and its corresponding cDNA (MDL3) were isolated from black cherry (*Prunus serotina*) and characterized. The mdl3 gene contains 2292 bp of the 5' flanking region, the entire coding region, and 300 bp of the 3' flanking region. The coding region is interrupted by three short introns, of which one possesses the unusual GC-AG splice junction dinucleotides. This gene encodes a polypeptide of 573 amino acids that includes a putative signal sequence, 13 potential N-glycosylation sites, and a presumptive FAD-binding site. To det. whether the 5' flanking region of the mdl3 gene is capable of driving MDL expression, it was fused to the .beta.-glucuronidase reporter gene for *Agrobacterium*-mediated transformation into tobacco. Matching endogenous MDL expression patterns, .beta.-glucuronidase staining was obsd. in maturing embryos and seeds; it also occurred in postembryonic tissues, esp. in assocn. with vascular tissues. After developing a homologous transient transformation system to facilitate identification of putative regulatory sequences, we demonstrated that 125 bp (-107 to +18) of the 5' flanking sequence of the mdl3 gene is sufficient for MDL expression in protoplasts derived from immature black cherry embryos.

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:142643 HCAPLUS

DOCUMENT NUMBER: 126:235180

TITLE: Molecular cloning of acetone cyanohydrin lyase from flax (*Linum usitatissimum*). Definition of a novel class of hydroxynitrile lyases

AUTHOR(S): Trummer, Klaus; Wajant, Harald

CORPORATE SOURCE: Institute of Cell Biology and Immunology, University of Stuttgart, Stuttgart, 70569, Germany

SOURCE: Journal of Biological Chemistry (1997), 272(8), 4770-4774

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Acetone cyanohydrin lyase from *Linum usitatissimum* is a hydroxynitrile lyase (HNL) which is involved in the catabolism of cyanogenic glycosides in young seedlings of

flax. The authors have isolated a full-length cDNA clone encoding L. usitatissimum HNL (LuHNL) from a cDNA expression library by immunoscreening. LuHNL cDNA was expressed in *Escherichia coli* and isolated from the resp. sol. fraction in an active form which was biochem. indistinguishable from the natural enzyme. An open reading frame of 1266 base pairs encodes for a protein of 45,780 kDa. The derived amino acid sequence shows no overall homologies to the to date cloned HNLs, but has significant similarities to members of the alc. dehydrogenase (ADH) family of enzymes. In particular, the cysteine and histidine residues responsible for coordination of an active site Zn²⁺ and a second structurally important Zn²⁺ in alc. dehydrogenases are conserved. Nevertheless, the authors found neither alc. dehydrogenase activity in LuHNL nor HNL activity in ADH. Moreover, well known inhibitors of ADHs, which interfere with the coordination of the active site Zn²⁺, fail to affect HNL activity of LuHNL, suggesting principally different mechanisms of cyanohydrin cleavage and alc. oxidn. Interestingly, LuHNL like ADH and *Prunus serotina* (PshNL) possesses an ADP-binding .beta..alpha..beta. unit motif, pointing to the possibility that the non-flavoprotein PshNL and the flavoprotein LuHNL have developed from two independent lines of evolution of a common ancestor with an ADP-binding .beta..alpha..beta. unit.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:811505 HCAPLUS

DOCUMENT NUMBER: 123:334898

TITLE: Temporal and spatial expression of amygdalin hydrolase and (R)-(+)-mandelonitrile lyase in black cherry seeds
 AUTHOR(S): Zheng, Liansheng; Poulton, Jonathan E.
 CORPORATE SOURCE: Dep. Biol. Sciences, Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1995), 109(1), 31-9

CODEN: PLPHAY; ISSN: 0032-0889

PUBLISHER: Dekker

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In black cherry (*Prunus serotina* Ehrh.) macerates, the cyanogenic diglucoside (R)-amygdalin undergoes stepwise degradn. to HCN catalyzed by amygdalin hydrolase (AH), prunasin hydrolase, and (R)-(+)-mandelonitrile lyase (MDL). A near full-length AH cDNA clone (pAH1), whose insert encodes the isoenzyme AH I, has been isolated and sequenced. AH I exhibits several features characteristic of .beta.-glucosidases of the BGA family, including their likely nucleophile center (isoleucine-threonine-glutamic acid-asparagine-glycine) and acid catalyst (asparagine-glutamic acid-proline/isoleucine) motifs. The temporal expression of AH and MDL in ripening fruit was analyzed by northern blotting. Neither mRNA was detectable until approx. 40 days after flowing (DAF), when embryos first became visible to the naked eye. Both mRNAs peaked at approx. 49 DAF before declining to negligible levels when the fruit matured (82 DAF). Taken together with enzyme activity data, these time courses suggest that AH and MDL expression may be under transcriptional control during fruit maturation. In situ hybridization anal. indicated that AH transcripts are restricted to the procambium, whereas MDL transcripts are localized within cotyledonary parenchyma cells. These tissue-specific distributions are consistent with the major locations of AH and MDL protein in mature seeds previously detd. by immunocytochem. (E. Swain, C.P.Li, and J.E. Poulton [1992] Plant Physiol 100:291-300).

L5 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:273430 HCAPLUS

DOCUMENT NUMBER: 122:51429

TITLE: Immunocytochemical localization of prunasin hydrolase and mandelonitrile lyase in stems and leaves of *Prunus serotina*

AUTHOR(S): Swain, Elisabeth; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1994), 106(4), 1285-91

PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In macerates of black cherry (*P. serotina*) leaves and stems, (R)-prunasin is catabolized to HCN, benzaldehyde, and D-glucose by the sequential action of prunasin hydrolase (E.C. 3.2.1.21) and (R)-(+)-mandelonitrile lyase (E.C. 4.1.2.10). Immunocytochem. techniques have shown that within these organs prunasin hydrolase occurs within the vacuoles of phloem parenchyma cells. In arborescent leaves, mandelonitrile lyase was also located in phloem parenchyma vacuoles, but comparison of serial sections revealed that these two degradative enzymes are usually localized within different cells.

L5 ANSWER 8 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:676851 HCAPLUS

DOCUMENT NUMBER: 121:276851

TITLE: Utilization of amygdalin during seedling development of *Prunus serotina*

AUTHOR(S): Swain, Elisabeth; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sciences, The Univ. of Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1994), 106(2), 437-45

CODEN: PLPHAY; ISSN: 0032-0889

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Cotyledons of mature black cherry (*P. serotina*) seeds contain the cyanogenic diglucoside (R)-amygdalin. The levels of amygdalin, its corresponding monoglucoside (R)-prunasin, and the enzymes that metabolize these cyanoglycosides were measured during the course of seedling development. During the first 3 wk following imbibition, cotyledonary amygdalin levels declined by >80%, but free hydrogen cyanide was not released to the atm. Concomitantly, prunasin, which was not present in mature, ungerminated seeds, accumulated in the seedling epicotyls, hypocotyls, and cotyledons to levels approaching 4 μmol per seedling. Whether this prunasin resulted from amygdalin hydrolysis remains unclear, however, because these organs also possess UDPG:mandelonitrile glucosyltransferase, which catalyzes de novo prunasin biosynthesis. The reductn. in amygdalin levels was paralleled by declines in the levels of amygdalin hydrolase (AH), prunasin hydrolase (PH), mandelonitrile lyase (MDL), and β -cyanoalanine synthase. At all stages of seedling development, AH and PH were localized by immunocytochem. within the vascular tissues. In contrast, MDL occurred mostly in the cotyledonary parenchyma cells but also present in the vascular tissues. Soon after inhibition, AH, PH, and MDL were found within protein bodies but were later detected in vacuoles derived from these organelles.

L5 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:47094 HCAPLUS

DOCUMENT NUMBER: 120:47094

TITLE: Cloning of cDNA of *Prunus serotina* (R)-(+)-mandelonitrile lyase and identification of a putative FAD-binding site

Cheng, I Ping; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant and Cell Physiology (1993), 34(7),

1139-43

CODEN: PCPHA5; ISSN: 0032-0781

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A full-length cDNA clone encoding the flavoprotein (R)-(+)-mandelonitrile lyase was isolated from a black cherry (*Prunus serotina*) cDNA expression library and sequenced. A putative FAD-binding site was identified near the N-terminus of this enzyme by comparing its deduced amino acid sequence with those of other FAD- and NAD-binding proteins.

L5 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:4491 HCAPLUS

DOCUMENT NUMBER: 120:4491
TITLE: Enzymology of cyanogenesis in rosaceous stone fruits
AUTHOR(S): Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: ACS Symposium Series (1992),
533(-Glucosidases), 170-90
CODEN: ACSMC8; ISSN: 0097-6156
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 43 refs. Mature black cherry (*Prunus serotina*) seeds accumulate the cyanogenic diglycoside (R)-amygdalin (the .beta.-gentiobioside of (R)-mandelonitrile). Upon tissue disruption, amygdalin is rapidly catabolized to HCN and benzaldehyde by the enzymes amygdalin hydrolase, prunasin hydrolase and mandelonitrile lyase. These glycoproteins were purified to homogeneity and their major kinetic and mol. properties characterized. Aspects of the temporal and spatial regulation of cyanogenesis in maturing cherry fruits were investigated using monospecific polyclonal antisera raised against each of the deglycosylated proteins. The three catabolic enzymes, which first appeared within developing seeds about six weeks after flowering, were localized at the tissue and subcellular levels by colloidal gold immunocytochem. Amygdalin hydrolase and prunasin hydrolase were found specifically within protein bodies of the procambium, while mandelonitrile lyase was primarily located within protein bodies of the cotyledonary parenchyma cells and with lesser amts. within the procambium. Amygdalin localization, which would reveal how premature cyanogenesis is avoided in undamaged seeds, is under investigation.

L5 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:630166 HCAPLUS
DOCUMENT NUMBER: 117:230166
TITLE: Tissue and subcellular localization of enzymes
catabolizing (R)-amygdalin in mature *Prunus serotina*
seeds
AUTHOR(S): Swain, Elisabeth; Li, Chun Ping; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1992), 100(1), 291-300
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In black cherry (*Prunus serotina*) homogenates, (R)-amygdalin is catabolized to HCN, benzaldehyde, and D-glucose by the sequential action of amygdalin hydrolase, prunasin hydrolase, and mandelonitrile lyase. The tissue and subcellular localizations of these enzymes were detd. within intact black cherry seeds by direct enzyme anal., immunoblotting, and colloidal gold immunocytochem. techniques. The two .beta.-glucosidases are restricted to protein bodies of the procambium, which ramifies throughout the cotyledons. Although amygdalin hydrolase occurred within the majority of procambial cells, prunasin hydrolase was confined to the peripheral layers of this meristematic tissue. Highest levels of mandelonitrile lyase were obsd. in the protein bodies of the cotyledonary parenchyma cells, with lesser amts. in the procambial cell protein bodies. The residual endosperm tissue had insignificant levels of amygdalin hydrolase, prunasin hydrolase, and mandelonitrile lyase

L5 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:252226 HCAPLUS
DOCUMENT NUMBER: 116:252226
TITLE: Development of the potential for cyanogenesis in
maturing black cherry (*Prunus serotina* Ehrh.) fruits
AUTHOR(S): Swain, Elisabeth; Li, Chun Ping; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1992), 98(4), 1423-8
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Biochem. changes related to cyanogenesis (HCN prodn.) were monitored during maturation of black cherry (*Prunus serotina*) fruits. At weekly intervals from flowering until maturity, fruits (or selected parts thereof) were analyzed for (a) fresh and dry wts., (b) prunasin and amygdalin levels, and (c) levels of the catabolic enzymes amygdalin hydrolase, prunasin hydrolase, and mandelonitrile lyase. During phase I (0-28 days after flowering [DAF]), immature fruits accumulated prunasin (mean: 3 μ mol/fruit) but were acyanogenic because they lacked the above enzymes. Concomitant with cotyledon development during mid-phase II, the seeds began accumulating both amygdalin (mean: 3 μ mol/seed) and the catabolic enzymes and were highly cyanogenic upon tissue disruption. Meanwhile, prunasin levels rapidly declined and were negligible by maturity. During phases II (29-65 DAF) and III (66-81 DAF), the pericarp also accumulated amygdalin, whereas its prunasin content declined toward maturity. Lacking the catabolic enzymes, the pericarp remained acyanogenic throughout all developmental stages.

L5 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:579400 HCAPLUS

DOCUMENT NUMBER: 115:179400

TITLE: Immunocytochemical localization of
mandelonitrile lyase in mature black
cherry (*Prunus serotina* Ehrh.)
seeds

AUTHOR(S): Wu, Hua Cheng; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1991), 96(4), 1329-37

CODEN: PLPHAY; ISSN: 0032-0889

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Mandelonitrile lyase (MDL, EC 4.1.2.10), which catalyzes the reversible disocn. of (R)-(+)-mandelonitrile to benzaldehyde and hydrogen cyanide, was purified to apparent homogeneity from mature black cherry (*P. serotina*) seeds by conventional protein purifn. techniques. This flavoprotein is monomeric with a subunit mol. mass of 57 kilodaltons. Glycoprotein character was shown by its binding to the affinity matrix Con A-Sepharose 4B with subsequent elution by α -methyl-D-glucoside. Upon chem. deglycosylation by trifluoromethanesulfonic acid, the mol. mass was reduced to 50.9 kilodaltons. Two-dimensional gel anal. of deglycosylated MDL revealed the presence of several subunit isoforms of similar mol. mass but differing slightly in isoelec. point. Polyclonal antibodies were raised in New Zealand white rabbits against deglycosylated and untreated MDL. Antibody titers were detd. by enzyme linked immunosorbent and dot immunobinding assays, while their specificities were assessed by Western immunoblot anal. Antibodies raised against untreated lyase recognized several proteins in addn. to MDL. In contrast, antisera raised against deglycosylated MDL were monospecific and were utilized for developmental and immunocytochem. localization studies. SDS-PAGE and immunoblotting anal. of seed proteins during fruit maturation showed that MDL first appeared in seeds shortly after cotyledons began development. In cotyledon cells of mature seeds, MDL was localized primarily in the cell wall with lesser amts. in the protein bodies, whereas in endosperm cells, this labeling pattern was reversed. N-terminal sequence data was gathered for future mol. approaches to the question of MDL microheterogeneity.

L5 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:225718 HCAPLUS

DOCUMENT NUMBER: 114:225718

TITLE: Purification, characterization, and immunocytochemical
localization of mandelonitrile lyase
from mature *Prunus serotina* seeds

AUTHOR(S): Wu, Hua Cheng

CORPORATE SOURCE: Univ. Iowa, Iowa City, IA, USA

SOURCE: (1990) 211 pp. Avail.: Univ. Microfilms

Int., Order No. DA9103280

From: Diss. Abstr. Int. B 1991, 51(9), 4153

DOCUMENT TYPE: Dissertation

LANGUAGE: English

AB Unavailable

L5 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:436548 HCAPLUS

DOCUMENT NUMBER: 111:36548

TITLE: Localization and catabolism of cyanogenic glycosides

AUTHOR(S): Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Ciba Foundation Symposium (1988),

140(Cyanide Compd. Biol.), 67-91

CODEN: CIBSB4; ISSN: 0300-5208

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 18 refs. The catabolism of cyanogenic glycosides is initiated by cleavage of the carbohydrate moiety by one or more .beta.-glycosidases, which yields the corresponding .alpha.-hydroxynitrile. Investigation of highly purified .beta.-glycosidases from plants contg. cyanogenic disaccharides has now indicated that these compds. may be degraded via 2 distinct pathways, depending on the plant species. .beta.-glycosidases from *Davallia trichomanoides* and *Vicia angustifolia* hydrolyzed (R)-vicianin and (R)-amygdalin at the aglycon-disaccharide bond producing mandelonitrile and the corresponding disaccharide. Alternatively, hydrolysis of cyanogenic disaccharides in *Prunus serotina*, almonds, and *Linum usitatissimum* involves stepwise removal of the sugar residues. The nature of these enzymes and of other .beta.-glycosidases responsible for hydrolysis of simple cyanogenic monosaccharides is discussed. Hydroxynitriles may decom. either spontaneously or enzymically in the presence of a hydroxynitrile lyase (I) to produce HCN and an aldehyde or ketone. The major kinetic and mol. properties of I purified from species accumulating arom. and aliph. cyanogens are reviewed. Cyanogenesis occurs rapidly only after cyanogenic plant tissues are macerated, allowing glycosides access to their catabolic enzymes. The possible nature of the compartmentation which prevents cyanogenesis under normal conditions is discussed in relation to tissue and subcellular localizations of cyanogens and catabolic enzymes.

L5 ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:420837 HCAPLUS

DOCUMENT NUMBER: 105:20837

TITLE: Isolation and characterization of multiple forms of mandelonitrile lyase from mature

black cherry (*Prunus serotina* Ehrh.) seeds

AUTHOR(S): Yemm, Robert S.; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Archives of Biochemistry and Biophysics (1986

), 247(2), 440-5

CODEN: ABBIA4; ISSN: 0003-9861

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Five multiple forms (forms 1-5) of mandelonitrile lyase (EC 4.1.2.10) which catalyze the decomn. of maldelonitrile to benzaldehyde and HCN were extensively purified from seeds of black cherry (*P. serotina*) by concanavalin A (Con A)-Sephrose 4B chromatog. and chromatofocusing. These forms were monomers which differed only slightly in mol. wt. (57,000-59,000) and pI (4.58-4.63), but heterogeneity in their carbohydrate side-chains was suggested by Con A-Sephrose 4B chromatog. The absorption spectra of the predominating forms 4 and 5 showed max. at 278, 380, and 460 nm, indicative of flavoprotein character. Detailed comparative kinetic studies of forms 4 and 5 revealed few significant differences in behavior. Both proteins showed pH optima between 6.0 and 7.0, had identical Km values (0.17 mM) for (R,S)-mandelonitrile, and retained similar activities upon storage at 4 and -20.degree.. Neither form exhibited a metal ion requirement, and both were affected similarly by metal salts, .beta.-mercaptoethanol, and SH-group reagents. Benzoic acid, p-hydroxybenzyl alc., and benzyl alc. inhibited both forms.

TITLE Hydroxy nitrile lyase activity, recombinant proteins with
JOURNAL J Biol Chem 271:10008-10012 (1996)
FEATURES DSF Fine Chemicals Austria Nfg GmbH & Co KG (AT)

Location/Qualifiers
1..2162
/organism="Prunus dulcis"
/db_xref="taxon:3755"

BASE COUNT 619 a 437 c 428 g 678 t
ORIGIN
100.0%; Score 2162; DB 6; Length 2162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAATTCAGATATGGGAATCAACAAATTCAGTATCTATCTATGTGTGCATCTCTT 60
DB 1 GGAATTCAGATATGGGAATCAACAAATTCAGTATCTATCTATGTGTGCATCTCTT 60
QY 61 GTCT 120
DB 61 GTCT 120
QY 121 TTTCGCT 180
DB 121 TTTCGCT 180
QY 181 CAGATGTCAGGACGACGATTAATTTAGATGCTGTTGATGCTGTTGATGCTGTTGAT 240
DB 181 CAGATGTCAGGACGACGATTAATTTAGATGCTGTTGATGCTGTTGATGCTGTTGAT 240
QY 241 TCATCATATTTTCAGATTTAGTACTGATGTTGTGACACACCCATGATACAG 300
DB 241 TCATCATATTTTCAGATTTAGTACTGATGTTGTGACACACCCATGATACAG 300
QY 301 CTCGAGGATCATATGATCTGATTAATGCTGTGAGGACATCAGGCTGTCATTGGC 360
DB 301 CTCGAGGATCATATGATCTGATTAATGCTGTGAGGACATCAGGCTGTCATTGGC 360
QY 361 AGCAATCTTATGAGAAATACAGGCTCTCTCTAGAGAGAGCATATGCTACAGA 420
DB 361 AGCAATCTTATGAGAAATACAGGCTCTCTCTAGAGAGAGCATATGCTACAGA 420
QY 421 ATACCGAGCACTGTACATGATGGTGTGCAATATCTCTGACGACACGATATG 480
DB 421 ATACCGAGCACTGTACATGATGGTGTGCAATATCTCTGACGACACGATATG 480
QY 481 AAAGACCCATGTAAAGGCTGTGTCGAGAGGCAATGATATGTGTCGAGCAGAT 540
DB 481 AAAGACCCATGTAAAGGCTGTGTCGAGAGGCAATGATATGTGTCGAGCAGAT 540
QY 541 CTTCTGTGCGACGACATTAATCAATGAGGCTCTGACGAGGCAATCTTATCTG 600
DB 541 CTTCTGTGCGACGACATTAATCAATGAGGCTCTGACGAGGCAATCTTATCTG 600
QY 601 TACTGTAAACAGATTCGATCAGCTGCTGTGTCGAGAGGCAATGATGATGCT 660
DB 601 TACTGTAAACAGATTCGATCAGCTGCTGTGTCGAGAGGCAATGATGATGCT 660
QY 661 AAGACGCTGTGTGACGACGATTAATCAATGAGGCTCTGACGAGGCAATCTT 720
DB 661 AAGACGCTGTGTGACGACGATTAATCAATGAGGCTCTGACGAGGCAATCTT 720
QY 721 CTTGAGGAGGCTTATCTCTGACATGATTAATTTTGTGTCGAGAGGCAATG 780
DB 721 CTTGAGGAGGCTTATCTCTGACATGATTAATTTTGTGTCGAGAGGCAATG 780
QY 781 ACTACCGGCTCAATTTTGCATTAATGACGATGATGATGATGATGATGATGAT 840
DB 781 ACTACCGGCTCAATTTTGCATTAATGACGATGATGATGATGATGATGATGAT 840
QY 841 TAAGAGGAGCCCTAATACCTGCTAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 900

DB 841 TAAGAGGAGCCCTAATACCTGCTAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 900
QY 901 CTTCTCCATCAATCAATGATGTCATCATGATATTAATGATGCTCTAGTTCG 960
DB 901 CTTCTCCATCAATCAATGATGTCATCATGATATTAATGATGCTCTAGTTCG 960
QY 961 ATGCTGCTAGTTCGATATTAATTTATCTATTAATTAATTAATTAATTAATTAAT 1020
DB 961 ATGCTGCTAGTTCGATATTAATTTATCTATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 CTTCTATTTTCCT 1080
DB 1021 CTTCTATTTTCCT 1080
QY 1081 GTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 GTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 ATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 ATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 ATGCTGCTAGGACGATTCGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGCTGCTAGGACGATTCGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GATGCTTACT 1320
DB 1261 GATGCTTACT 1320
QY 1321 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 CATTCTTCCATCAGCTTCTGATGCTTTTCTTCTACACATCTTACCCCTCCCAATTC 1500
DB 1441 CATTCTTCCATCAGCTTCTGATGCTTTTCTTCTACACATCTTACCCCTCCCAATTC 1500
QY 1501 ACTTTTCT 1560
DB 1501 ACTTTTCT 1560
QY 1561 AATTCATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 AATTCATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 ACAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 ACAGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 GTACCTTCTCCAGGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 GTACCTTCTCCAGGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 GTAGCT 1860
DB 1801 GTAGCT 1860
QY 1861 TTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
DB 1861 TTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1921 CCAAGAGGACCTTCT 1980
DB 1921 CCAAGAGGACCTTCT 1980

[illegible]

Dd 123 ACTGTAAGATTGTGTACACAGCCGACATGACAGCTTGGAGAGTCAATATGACTACATNTG 182
 Qy 327 TAATCGGTGGAGACATCAGGGCTGCTGATGACACACATTTATTCGAGAAATCAAGG 386
 Dd 183 TAATCGGTGGAGACATCAGGGCTGCTGATGACACACATTTATTCGAGAAATCAAGG 242
 Qy 387 TGGCTTCTTACAGAGAGCAGCTATGCTTACAGAAATCCGAGACAGCTGCGAGATG 446
 Dd 243 TGGCTTCTTACAGAGAGCAGCTATGCTTACAGAAATCCGAGACAGCTGCGAGATG 302
 Qy 447 GCTTCCGCTATATTCGAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
 Dd 303 GCTTCCGCTATATTCGAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 362
 Qy 507 CGAGAGTCGCTATATTCGAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
 Dd 363 CGAGAGTCGCTATATTCGAGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
 Qy 567 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
 Dd 423 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
 Qy 627 TATGTTTGGTCAATGATGATGAGTGGTGTGAAGAGAGAGATCTTGGAGCGGATTTCTCC 686
 Dd 483 TGGATTTGGTCAATGATGATGAGTGGTGTGAAGAGAGAGATCTTGGAGCGGATTTCTCC 542
 Qy 687 ATCAATCTTGGCATCTGTTATGAGAGAGAGATCTTGGAGCGGATTTCTCCGACGA 746
 Dd 543 ATCAATCTTGGCATCTGTTATGAGAGAGAGATCTTGGAGCGGATTTCTCCGACGA 602
 Qy 747 ATGATTTAGTTTGGATGACAGAGCAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
 Dd 603 ATGATTTAGTTTGGATGACAGAGCAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
 Qy 807 ATGACACGACATCGGGCTGATGATCTGCTGATTAAGAGAGCCTTATTAACCTGCTAG 866
 Dd 663 ATGACACGACATCGGGCTGATGATCTGCTGATTAAGAGAGCCTTATTAACCTGCTAG 722
 Qy 867 TTGCAGTTCAGGCTCAGTACAGAGATCTTCTTCTTCCATCATCAAGTATGCTG 926
 Dd 723 TTGCAGTTCAGGCTCAGTACAGAGATCTTCTTCTTCCATCATCAAGTATGCTG 773
 Qy 927 ATCATGATATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 986
 Dd 774 ATCATGATATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
 Qy 987 ATCATTTTAATTTACAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
 Dd 774 ATCATTTTAATTTACAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
 Qy 1047 ATTTCCTATCAACAACTCCCATMTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
 Dd 774 ATTTCCTATCAACAACTCCCATMTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
 Qy 1107 ATTCTTATGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1166
 Dd 774 ATTCTTATGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
 Qy 1167 TATGAGCAATTTGAGGGTACAGAGAGATTTATGATGATGATGATGATGATGATGATGAT 1286
 Dd 820 TATGAGCAATTTGAGGGTACAGAGAGATTTATGATGATGATGATGATGATGATGATGAT 879
 Qy 1227 GCTCAGCTTCTATCTATGAGGGTGGAGAGAGATTTATGATGATGATGATGATGATGATG 1346
 Dd 880 GCTCAGCTTCTATCTATGAGGGTGGAGAGAGATTTATGATGATGATGATGATGATGATG 939
 Qy 1347 CATTTATTTTGGCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 999
 Dd 1347 CATTTATTTTGGCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1406
 Qy 1000 CATTTATTTTGGCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1059

Qy 1407 AATGATATTTATCAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1466
 Dd 1060 AATGATATTTATCAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1119
 Qy 1119 TTTTTCATCAATTTATCAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1526
 Dd 1120 TTTTTCATCAATTTATCAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1579
 Qy 1527 TCGAGACATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1586
 Dd 1180 TCGAGACATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1239
 Qy 1587 TCGAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 1646
 Dd 1240 TCGAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 1299
 Qy 1647 CATGAGAGAGCTTGGTGAATTTATTAAGGACAAGCAATAGAACATTAATTAAGCTCGGA 1706
 Dd 1300 CATGAGAGAGCTTGGTGAATTTATTAAGGACAAGCAATAGAACATTAATTAAGCTCGGA 1359
 Qy 1707 TGTGCTGGGAATTAAGCTGTTCAATTTATTTGGAGTACTTTCGCGAGACCAACAG 1766
 Dd 1360 TGTGCTGGGAATTAAGCTGTTCAATTTATTTGGAGTACTTTCGCGAGACCAACAG 1419
 Qy 1767 TATGATGCTTTCGGAACATTTTATGATTTAGTATTTAGTCTTATGAGCTTATACAG 1826
 Dd 1420 TATGATGCTTTCGGAACATTTTATGATTTAGTATTTAGTCTTATGAGCTTATACAG 1479
 Qy 1827 TGGAGAGCTTGGTGGAGAGTCTGATGACAGTTCCTGCTGATTTGGGATCAAGCAAT 1886
 Dd 1480 TGGAGAGCTTGGTGGAGAGTCTGATGACAGTTCCTGCTGATTTGGGATCAAGCAAT 1539
 Qy 1887 ACGGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1946
 Dd 1540 ACGGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1599
 Qy 1947 TGTGAGCTTGGAGAGTATGATG 1968
 Dd 1600 TGTGATTTGATGAGGATTTG 1621

RESULT 4
 AX174397
 LOCUS Sequence 21 from Patent EP1223220.
 DEFINITION AX174397
 ACCESSION AX174397.1 GI:22214002
 VERSION 1
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 1 artificial sequences.
 REFERENCE
 AUTHORS Schwab R., Glieder A., Kracky C., Dreveny I., Poeschlauer P., Strano W., Mayrhofer H., Wirth, I., Neuhofer R. and Bona R.
 TITLE Genes coding for hydroxybutyrate lyase, recombinant proteins with hydroxybutyrate lyase activity and their use
 JOURNAL Patent: EP 1223220-A 21.17-JUN-2002
 FEATRES
 source
 location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="PAMHUSXGX"
 BASE COUNT 451 a 357 c 361 g 463 t
 ORIGIN

Query Match 58.8%; Score 1272; DB 6; Length 1632;
 Desc Local Similarity 88.0%; Pred. No. 8.4e-280;
 Matches 1469, Conservative 0; Mismatches 0; Indels 203; Gaps 1;
 Qy 281 TACAGCCCATGATCAAGCTCGGAGAGCATATGATGACTACTATGTTGATCGTGGAGCA 340

PC CL2N15/09, C07K19/00, CL2N9/04, CL2N9/88, CL2P13/00, CL2N15/00 CC
Description of the artificial sequence: PAMN155G0X PH Key

Location/Qualifiers
FT source 1.1632 /organism="synthetic construct"

FEATURES
source 1.1632 /organism="synthetic construct"

BASE COUNT 451 a 357 c 361 g 463 t

ORIGIN
Query Match 58.8%; Score 1272; DB 6; Length 1632;
Best Local Similarity 88.0%; Pred. No. 8.4e-280; Gaps 1;
Matches 1485; Conservative 0; Mismatches 0; Indels 203;

281 TACAGCCGACCTATACAGAGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 140
Db TACAGCCGACCTATACAGAGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 153

341 AGATCGAGGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 400
Db AGATCGAGGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 413

154 ACATCGAGGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 213
Db ACATCGAGGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 226

401 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 460
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 473

214 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 273
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 286

461 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 520
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 533

274 CTGACAGCAGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 333
Db CTGACAGCAGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 346

521 GATATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 580
Db GATATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 593

581 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 640
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 653

394 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 453
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 466

641 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 700
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 713

454 AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 513
Db AGAGCGATCGATGCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 526

701 TCTGATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 760
Db TCTGATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 773

514 TCTGATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 573
Db TCTGATATGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 586

761 GATACAGCAGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 820
Db GATACAGCAGAGGATCGAGAGGATCATATATGATCTATGATCTGCGTGGGA 833

821 GCGGCTGATGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 880
Db GCGGCTGATGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 893

634 GCGGCTGATGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 693
Db GCGGCTGATGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 706

881 TACAGAGAGAGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 940
Db TACAGAGAGAGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 953

694 TACAGAGAGAGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 753
Db TACAGAGAGAGATCTCTTATATGAGGATCATATATGATCTATGATCTGCGTGGGA 766

941 ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000
Db ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013

731 ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790
Db ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803

1001 CTACAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060
Db CTACAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1073

731 ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790
Db ATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803

1061 AACCTCCCAATCT 1120
Db AACCTCCCAATCT 1133

QY 1121 ATTCTGACGATATTGAGATCATATATGAGGATCTGATGAGAACTCTCATCAGCAATTG 1180
Db 1131 ATTCTGACGATATTGAGATCATATATGAGGATCTGATGAGAACTCTCATCAGCAATTG 1190

QY 781 TATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 791 TATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850

QY 1241 TACTTATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1300
Db 1251 TACTTATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1310

QY 851 TACTTATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
Db 861 TACTTATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 920

QY 1301 GATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
Db 1311 GATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1370

QY 1361 CCCCAATCCATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1420
Db 1371 CCCCAATCCATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1430

QY 1421 AGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1480
Db 1431 AGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1490

QY 1481 CTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1540
Db 1491 CTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1550

QY 1541 CTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1600
Db 1551 CTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1610

QY 1661 TCAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1720
Db 1671 TCAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1730

QY 1721 AGGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780
Db 1731 AGGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1790

QY 1331 AGGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390
Db 1341 AGGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1400

QY 1781 AACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
Db 1791 AACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1850

QY 1841 GGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
Db 1851 GGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1910

QY 1451 GGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510
Db 1461 GGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520

QY 1511 CTTCAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1570
Db 1521 CTTCAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580

QY 1571 GGTATGATG 1578
Db 1581 GGTATGATG 1588

RESULT 6
PBUT8814
LOCUS

DEFINITION
Prunus serotina (R.) (-)-mandelonitrile lyase isoform MDU1 precursor

ACCESSION
U78814.1

VERSION
U78814.1 GI:1703031

KEYWORDS
Prunus serotina (black cherry)

SOURCE
Bakery; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORGANISM
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

248 TATTTCGAGATTAGCTACTGAGTTTGTGCAAGCGCACTGATCAAGCTGGAA
307
240 GATTTCAGATTAACTCACTGACCTTTGATACAGCGCTCTCTTAGAGTGGAA
289
308 GAGTATCTGACTACATCTTATCGTGGAGAACTACAGGTGTCTGATGGCACT
367
306 GATCTATGACTAGTATATGTTGTCGAGGAACATCTGATGGTGGCACT
359
368 TATCGAATAATCAAGAGTGTCTCTTCGAGAAAGGCTGATGCTACAGATACCG
427
360 TATCGAATAATCAAGAGTGTCTCTTCGAAAGGGGAGCTCTCGAGCAATACC
419
428 AACACCTTACTCGAGTGGTGTGATATCTGCAACAGAGTGGGAGAGCG
487
420 AAGCTGTGATGATGGGTTTGTATATCTTCCACAGAGATGGAAGACA
479
488 CAGTTGGAAGTGTGGTGGAGAGGATGATGATGAGGAGCGAGCTCGGT
547
480 CGGTGCGAAGGTTCTGATCCGAGATAGTATGTAATGTACGGGAGAGTCTCGGT
539
548 GEGCACTCATATCATCTCAGCGCTCTACCGCACTCAATCTCTATGATGCA
607
540 GGCACAGCAATGATATCCGCGTGTCTACCGCACTCAATCTCTATGATGCA
599
608 ACGGATATGATGCGGCTCATATGAGATGATGAGATGAGCTGTGGAGAGCC
667
600 TCGAGGATGATGGGACATGGATTTGGTTATCTGAGCACTATGGTGTGTGAGCACT
659
668 ATTGGTGTGACCAATATATGATCTGGGATCTGATATGAGAGAGGATATTGGAG
727
660 ATTGTATCAGCAAAATCTCAATCTGGAGCTGTTACAAAACTGATCTGGAG
719
728 CGGAGTCTTACGACATGATATGTTTGGATTCGACAGAGCGAGCACTGATCC
787
720 GCTGAGTCTTACATACCAAGCAAGGATGATGATGATGATGATGATGATGATGAT
779
788 GCTGACATTTGATCATATGAGCAAGGATGATGATGATGATGATGATGATGATGAT
847
780 GATCATTTTTCGACAGGAGGATGATGATGATGATGATGATGATGATGATGATGAT
839
848 GACCTATATCTCTAGTGTAGTCTCAGCGCTCAGTGGAGAGATCTCTCTCTCC
907
840 CATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
896
908 AATCATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
967
897 AAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
922
968 ACTCGAAATATATATTTATCATTTAAATATCTAACAGATAGTGGAGCTGATAT
1027
928 ACTCAAAATATATATGATTTGATATGATAGTGTACAGTACAGAGAGCTGAGAT
980
1028 TTCCCTTCATATTCGCAATTTCCATPACAAATCCCAATCTTCCTGCTTTAGT
1087
981
1088 TTGACATATATATAGCTATCTCTATGACAGATTTGGTCACTATGGAGTCAATATA
1147
1015 TTGATATGATATATAGCTATCTCTGATATGATAGTGTACAGTACAGAGATATATA
1074
1148 CGGATCTGATGAGAGATCTCAAGGATTTAGTACGCTGACGAGAGATATATATTA
1207
1075 GGGATCTTATGGAAGCTCTCAAGATTTTGAACGATAGAGAGATATATCTGTA
1134
1208 GTTCGAGGCAATCGAGAGCTCAGCTGATCTATCTATGAGTGGGTGCGAGAGCT
1267
1135 GTTCGAGGCAATCGAGAGCTCAGCTGATCTATCTATGAGTGGGTGCGAGAGCT
1194
1268 ACCGATGCTGATCAATGAGAGCTGATCTATCTATGAGTGGGTGCGAGAGCT
1327
1195 ACCTATCTCTATATATCAGTGTGTATGATGATGATGATGATGATGATGATGATGAT
1254
1269

[illegible]

BD18194	2087 bp	DNA	linear	PAT 15-MAY-2003
BD18194		containing	containing	
LOCUS		phage	phage	
DEFINITION		phage	phage	
		recombinant protein	recombinant protein	
		originating in the	originating in the	
		gene and having	gene and having	
		hydroxymethyl	hydroxymethyl	
		lyase activity and	lyase activity and	
		utilization thereof.	utilization thereof.	
ACCESSION	GI:30792832			
VERSION	2002.03.07			
KEYWORDS	UP 2002.03.07			
SOURCE	Prunus dulcis (almond)			
ORGANISM				
	Eubacteriales; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotids;			
	Rosales; eutroids I; Rosales; Rosaceae; Amygdaloideae; Prunus.			
REFERENCE				
AUTHORS	Schäfer, H., Giesecke, A., Krt'ek, V., D'Amico, I., Bon, R., Beltraval, P.,			

Db 497 TTGATGGGTTGTCTATGATCATCTCGAGCAACAGATGATGGAAGACACACGTCGAAGGTT 556
 Qy 501 TGTGTCCGAGATGCGCATGATTAATGTCGAGCGCGAGATCTCGGTGCGACACATAA 560
 Db 557 TATGTTCTCGAAGATGATTAATGATTAATGAGACGAGATCTCGGTGCGACACATAA 616
 Qy 561 TCGATGCGCTCTGATCGATGCGATGATGATGATGATGATGATGATGATGATGATGAT 620
 Db 617 TCAATGATGCGCTTATGTCGACAGCTATACGAGCTCATTTATTAATTAATGAGGCTGAT 676
 Qy 621 GCGATCGGATTTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
 Db 677 GCGATCGGATTTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
 Qy 681 CATATATCATGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
 Db 737 CAGATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 800
 Qy 741 CAGATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 856
 Db 797 CCGATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 856
 Qy 801 CATATATCATGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
 Db 857 ACGATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 916
 Qy 861 TCGATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 920
 Db 917 TGAATGATCAATCTTGCATCTATTAAGAGATGATGATGATGATGATGATGATGATGAT 976
 Qy 921 TGTGTCATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980
 Db 977 TGTGTCATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 Qy 981 TATTTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1040
 Db 1027 TATTTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1071
 Qy 1041 TTCCGAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1100
 Db 1072 -----AAGTGTTAATCATAGTTA 1090
 Qy 1101 TAACGATTCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1160
 Db 1091 TAAGTATTCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1150
 Qy 1161 AAGCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1220
 Db 1151 AAGCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1210
 Qy 1221 CCGATGATTCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1280
 Db 1211 CCGATGATTCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1270
 Qy 1281 CAGATGATTCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1340
 Db 1271 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1330
 Qy 1341 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1400
 Db 1331 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1390
 Qy 1401 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1460
 Db 1391 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1450
 Qy 1461 TATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1520
 Db 1451 CATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1510
 Qy 1521 CATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1580

Db 1511 CAAGATGCTCGAGACTTATCTGCTGTGTAGTCTGACTCTGAGATCATCTCTAATGTGAG 1570
 Qy 1551 AATGCTGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1640
 Db 1571 GGTGCGACCAATGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1630
 Qy 1641 TAGGCGGTGAGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1700
 Db 1631 TAGGCGGTGAGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1690
 Qy 1701 TCGAGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1760
 Db 1691 TCGAGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1750
 Qy 1761 AAGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1820
 Db 1751 AAGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1810
 Qy 1821 CCGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1880
 Db 1811 CCGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1870
 Qy 1881 AAGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1940
 Db 1871 TCGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1930
 Qy 1941 CTTGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1996
 Db 1931 CTTGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 1980
 Qy 1997 GAGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 2042
 Db 2042 TTTGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 2102
 Qy 2051 TTTGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 2050
 Db 2103 GAGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 2108
 Db 2109 GAGATGATGCTCGAGAGCTTGTGAGTACTTATTAAGGACCAAGGAGCTATAGAACATTAAGC 2141

RESULT 12
 AF053885
 LOCUS Prunus serotina (R)-(-)-mandelonitrile lyase isoform MDL4 precursor
 DEFINITION Prunus serotina (R)-(-)-mandelonitrile lyase isoform MDL4 precursor
 ACCESSION AF053885
 VERSION AF053885.1
 KEYWORDS Prunus serotina (black cherry)
 ORGANISM Prunus serotina (black cherry)
 SOURCE Prunus serotina (black cherry)
 REFERENCE Bukacinski, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.
 AUTHORS Hu, Z. 2000
 TITLE Direct Submission
 JOURNAL Submitted (17-MAR-1998) Biological Sciences, The University of
 Iowa, Iowa City, IA 52242, USA
 FEATURES
 source 1..2380
 locus/qualifiers 1..2380
 /organism="Prunus serotina"
 /mol_type="genomic DNA"
 db_xref=taxon:232074
 /gene="MDL4"
 join(1..132,314..973,1111..1951,2084..2380)
 /gene="MDL4"
 /gene="MDL4"
 join(27..132,314..973,1111..1951,2084..2201)
 CDS

[illegible]

QY 1347 CHTAATNTTGGCCCAATCAATCAATAGGCTCTGTGTAACGTGTTAGGONTAG 1406
 Db 1005 CATTACATTTGGCCCAATCAATCAATAGGCTCTGTGTAACGTGTTAGGONTAG 1064
 QY 1407 AGTGAATATATCAAGCTTCTCTGTGTAACGTGTTAGGONTAG 1466
 Db 1065 AGTGAATATATCAAGCTTCTCTGTGTAACGTGTTAGGONTAG 1124
 QY 1467 TTTCTCAACATCTTACCCCTCCCAATTCGACTTTGCTCATATTTAGCAAGT 1526
 Db 1125 TTTCTCAACATCTTACCCCTCCCAATTCGACTTTGCTCATATTTAGCAAGT 1184
 QY 1527 TCCAGACCATTTGCTGTCGCTCACTAAATTCATCATCTGAGTGGAGTCC 1586
 Db 1185 TCCAGACCATTTGCTGTCGCTCACTAAATTCATCATCTGAGTGGAGTCC 1244
 QY 1587 TCCAAATTAATTAATTAATTAATTAATTCAGAGCTTCTGTAATTTAGTCCG 1646
 Db 1245 TCCAAATTAATTAATTAATTAATTAATTCAGAGCTTCTGTAATTTAGTCCG 1304
 QY 1647 CAYGAGAGCTTGTGAGTATTAGGACAAAGGCAATAGAACCTATATAAGTTCAGA 1706
 Db 1305 CAYGAGAGCTTGTGAGTATTAGGACAAAGGCAATAGAACCTATATAAGTTCAGA 1364
 QY 1707 TGTGCTGGAAATTCAGGCTTCAATTTTGGAGTACTTTGCGAGACCAACAGGA 1766
 Db 1365 TGTGCTGGAAATTCAGGCTTCAATTTTGGAGTACTTTGCGAGACCAACAGGA 1424
 QY 1767 TGAAGTACTCTCGAAGCTTTGTGCTGAGTAAAGTACTTGTGCGAGACCAACAGGA 1826
 Db 1425 TGAAGTACTCTCGAAGCTTTGTGCTGAGTAAAGTACTTGTGCGAGACCAACAGGA 1484
 QY 1827 TCGAAGCTTGTGGAAGCTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1886
 Db 1485 TCGAAGCTTGTGGAAGCTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1544
 QY 1887 ACCGCTGTTGTAAGCTTGTGTAAGCTTGTGTAAGCTTGTGTAAGCTTGTGTAAG 1946
 Db 1545 ACCGCTGTTGTAAGCTTGTGTAAGCTTGTGTAAGCTTGTGTAAGCTTGTGTAAG 1604
 QY 1947 TTTGATTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1968
 Db 1605 TTTGATTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1626

Search completed: December 18, 2003, 17:26:57
 Job time : 7875 secs

GenCore version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 15:05:47 (Search time 4536 Seconds)

(without alignments)
11609.871 Million cell updates/sec

Title: US-10-046-232-19

Perfect score: 2162

Sequence: 1 ggaatccacatgagaa.....agtcctatggaatccg 2162

Scoring table:

Gapop 11.0, Gapext 1.0

22781392 seqs, 1215228056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em.esbta.*

2: em.esbta.*

3: em.esbta.*

4: em.esbta.*

5: em.esbta.*

6: em.esbta.*

7: em.esbta.*

8: em.esbta.*

9: em.esbta.*

10: gb.esbta.*

11: gb.esbta.*

12: gb.esbta.*

13: gb.esbta.*

14: gb.esbta.*

15: em.esbta.*

16: em.esbta.*

17: em.esbta.*

18: em.esbta.*

19: em.esbta.*

20: em.esbta.*

21: em.esbta.*

22: em.esbta.*

23: em.esbta.*

24: em.esbta.*

25: em.esbta.*

26: em.esbta.*

27: em.esbta.*

28: gb.esbta.*

29: gb.esbta.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454.2	77.0	60	BUS73954 PA_Ea000	
2	451.8	20.9	639	BUS71120 PA_Ea000	
3	438.6	20.3	654	BUS75280 PA_Ea000	
4	423.6	19.6	648	BUS74474 PA_Ea000	

5	394.6	18.3	640	13	BUS75069 PA_Ea000
6	392	18.1	658	13	BUS72973 PA_Ea000
7	383.4	17.7	598	13	BUS45516 EST789 a1
8	382.4	17.6	598	13	BUS45516 EST789 a1
9	358.2	16.6	634	13	BUS74792 PA_Ea000
10	317.2	14.7	656	13	BUS74699 PA_Ea000
11	317.2	14.6	595	13	BUS74357 PA_Ea000
12	314.8	14.6	595	13	BUS74357 PA_Ea000
13	242.6	11.2	621	13	BUS74592 PA_Ea000
14	185.4	8.6	543	13	BUS72781 PA_Ea000
15	143.8	6.7	503	13	BQ106017 FC1256 e
16	135.4	6.3	658	13	BQ61641 OG12002
17	135.4	6.3	658	13	BQ61641 OG12002
18	132.7	5.9	620	13	BQ15066
19	127	5.9	644	28	BH646279 BOND181TR
20	126.2	5.8	619	14	CA838661 NC7019A07
21	125.6	5.8	461	13	BQ104033 CO8856 e
22	125.6	5.8	461	13	BQ104033 CO8856 e
23	124.4	5.8	601	13	BQ682220 OG23012
24	124	5.7	561	12	B1211954 IP1 62 B1
25	116.8	5.4	716	29	BZ480736 BOMF28TR
26	116.8	5.4	716	29	BZ480736 BOMF28TR
27	114	5.3	905	10	BZ76508
28	112.2	5.2	555	14	CB092375 B107809-3
29	111	5.1	680	13	BQ999109 OG221C06
30	111	5.1	680	13	BQ999109 OG221C06
31	108.4	5.0	568	13	BQ986701 NC81 107
32	107.4	5.0	570	14	CB090460 975606-9
33	107.4	5.0	588	12	BZ247330 BZ247330
34	107.4	5.0	622	12	B1927379 EST574268
35	107.4	5.0	622	12	B1927379 EST574268
36	107.2	5.0	893	10	BZ278786 GA_Ea009
37	105	4.9	669	13	BQ406738 GA_Ea009
38	101.6	4.7	734	28	BH528838 BQHE087R
39	101.6	4.7	734	28	BH528838 BQHE087R
40	100.2	4.6	658	13	CB01125
41	99.2	4.6	649	13	BQ000407
42	97.2	4.5	782	28	BH668366 BQAL80TR
43	96.2	4.5	800	AL506828	
44	94.2	4.3	800	AL506828	
45	92	4.3	393	9	AU225001 AU225001

ALIGNMENTS

RESULT 1

LOCUS BUS73954

DEFINITION PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

ACCESSION BUS73954

KEYWORDS EST

SOURCE Prunus dulcis (almond)

ORGANISM Prunus dulcis

REFERENCE 1 (bases 1 to 640)

AUTHORS Dandekar,A., Main,D., Wing,R. and Abbott,A.

JOURNAL Unpublished

COMMENT Contact: Abbott, A.

DEPT of Genetics and Biochemistry

Clemson University

Clemson University, Clemson, SC 29634, USA

Phone: 864 656 3060

Fax: 864 656 6879

Email: albert@clcmson.edu

Internet: High Quality Sequences

Source: NCBI/BLAST/GenBank

High quality sequence stop: 640.

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea0005M16f Almond developing seed Prunus dulcis cDNA clone

FEATURES
SOURCE

Location/Qualifiers
1..640
/organism="Prunus dulcis"
/mol_type="mRNA"
/db_xref="taxon:3755"
/clone="PA_Ea000619f"
/tissue_type="embryo"
/clone_1ib="Almond developing seed"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
synonym: Prunus amygdalus"
BASE COUNT 187 a 123 c 160 g 169 t 1 others

Query Match 21.04; Score 454.2; DB 13; Length 640;
Best Local Similarity 81.74; Pred. No. 2.1e-83;
Matches 525; Conservative 0; Mismatches 99; Indels 2; Gaps 1;
Qy 257 GATTTCCTACTGAGTTGTGTGAAGCGCAGCTGATACAGCTGGAGAGATCATAT 316
Db 15 GATTTCCTACTGAGTTGTGTGAAGCGCAGCTGATACAGCTGGAGAGATCATAT 74
Qy 317 GACTACATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
Db 75 GACTACATGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 134
Qy 375 AAAATATCAAGAGTCT 434
Db 135 AAAATATCAAGAGTCT 194
Qy 435 TCACTCAGATGGT 494
Db 195 TCACTCAGATGGT 254
Qy 495 AAGGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
Db 255 AAGGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 314
Qy 555 CAT 614
Db 315 CAT 374
Qy 615 TTAG 674
Db 375 TTAG 434
Qy 675 TTAG 734
Db 435 TTAG 494
Qy 735 TTAG 794
Db 495 TTAG 554
Qy 795 TTAG 854
Db 555 TTAG 614
Qy 855 ATACT 914
Db 615 ATACT 674

RESULT 2
LOCUS 639 bp mRNA linear EST 17-SEP-2002
DEFINITION PA_Ea000619f Almond developing seed Prunus dulcis cDNA clone
ACCESSION BU574120
KEYWORDS EST/74120.1 GI:23032945
SOURCE Prunus dulcis (almond)

ORGANISM

Prunus dulcis

Rubycory; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosid 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
Dundekar A Main D., Wing R. and Abbott A.
Development of a Functional Genomics Database for Peach
Unpublished
JOURNAL CONTACT: Abbott, A.
COMMENT: Dundekar A, Wing R, and Abbott A.
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel.: 864 656 3060
Fax: 864 656 3061
Email: albert@clemson.edu

Total High Quality bases = 615
Seq primer: TAATCACTCACTACTAGG
High quality sequence length: 639.
Location/Qualifiers
1..639
/organism="Prunus dulcis"
/mol_type="mRNA"
/db_xref="taxon:3755"
/clone="PA_Ea000619f"
/tissue_type="embryo"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
synonym: Prunus amygdalus"
BASE COUNT 171 a 149 c 119 g 200 t

FEATURES
SOURCE

Query Match 20.94; Score 451.8; DB 13; Length 639;
Best Local Similarity 81.74; Pred. No. 6.6e-83;
Matches 522; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Qy 1315 GGGCAGTTTGTGTATGATCATCTCTGTATTTCTATTTATTTGCCCCCAATCCATT 1374
Db 1 GGGCAGTTTGTGTATGATCATCTCTGTATTTCTATTTATTTGCCCCCAATCCATT 60
Qy 1375 GAAGCTCTGTGTGACCTGTTTGTAGCATTAGAGATGATATATCAAGTTCTCTGCA 1434
Db 61 GAAGCTCTGTGTGACCTGTTTGTAGCATTAGAGATGATATATCAAGTTCTCTGCA 120
Qy 1435 ACCTGCATATCTTCCATCCATCCCTTATGTTTCTTCTACAGATCTACAGCTCCCA 1494
Db 121 ACCTGCATATCTTCCATCCATCCCTTATGTTTCTTCTACAGATCTACAGCTCCCA 180
Qy 1495 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1554
Db 181 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Qy 1555 ACCTGCATATCTTCCATCCATCCCTTATGTTTCTTCTACAGATCTACAGCTCCCA 1614
Db 241 ACCTGCATATCTTCCATCCATCCCTTATGTTTCTTCTACAGATCTACAGCTCCCA 300
Qy 1615 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1674
Db 301 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 1675 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1734
Db 361 AATTGCTTCTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 1735 TTGGAGTACTCTCCAG 1794
Db 421 TTGGAGTACTCTCCAG 480
Qy 1795 GATATGAGTCTCTATCTGGATATACAGCTGGAGAGCTTGTGGAGAGCTCTAAT 1854
Db 481 GATATGAGTCTCTATCTGGATATACAGCTGGAGAGCTTGTGGAGAGCTCTAAT 540


```

QY 1363 CCAATTCGATTCGAGCCTCTGTTTAACTGTTTAAAGCATTAGAGTATATATCA 1422
Db 1364 /organism="Prunus dulcis"
QY 1423 CTTATCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1482
Db 1424 /mot_type="mRNA"
QY 1425 CCAATTCGATTCGAGCCTCTGTTTAACTGTTTAAAGCATTAGAGTATATATCA 61
Db 1426 /cutter="NdeI"
QY 1427 CTTATCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1482
Db 1428 /clone="PA_EA000918f"
QY 1429 CTTATCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1482
Db 1430 /tissue_type="embryo"
QY 1431 CTTATCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1482
Db 1432 /lab_host="S. coli"
QY 1433 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1434 /clone="Prunus amygdalus"
QY 1435 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1436 /development="developing seed"
QY 1437 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1438 /site="ECOR1, Site 2: XhoI;"
QY 1439 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1440 /synonym="Prunus amygdalus"
QY 1441 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1442 /base_count 171 a 151 c 115 g 203 t
QY 1443 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1444 /quasi_match 18.3%; score 394.6; db 13; length 640;
QY 1445 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1446 /best_local_similarity 82.1%; pred. no. 4.4e-71;
QY 1447 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1448 /matches 454; conservative 0; mismatches 99; indels 0; gaps 0;
QY 1449 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1450 /qy 1118 CAGATTTTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1177
Db 1451 /db 87 CAGATTTTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1452 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1453 /qy 1178 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1237
Db 1454 /db 1176 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1455 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1456 /qy 1177 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1237
Db 1457 /db 1176 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1458 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1459 /qy 1238 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1297
Db 1460 /db 1176 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1461 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1462 /qy 207 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 266
Db 1463 /db 1298 AGCGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 326
QY 1464 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1465 /qy 1297 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1297
Db 1466 /db 1298 AGCGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 326
QY 1467 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1468 /qy 1297 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1297
Db 1469 /db 1298 AGCGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 326
QY 1470 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1471 /qy 1358 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1417
Db 1472 /db 327 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 386
QY 1473 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1474 /qy 1418 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1477
Db 1475 /db 387 ACATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 446
QY 1476 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1477 /qy 1478 CACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1537
Db 1478 /db 447 CACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 506
QY 1479 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1480 /qy 1538 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1597
Db 1481 /db 507 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 626
QY 1482 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1483 /qy 1598 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 566
Db 1484 /db 567 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 626
QY 1485 TACCCCTCCCAATTCGACTTTTCTCAATTCGAGTTCAGAGTTCAGAGTTCAGAGTTC 1542
Db 1486 /qy 1658 TTGTCGACTTAT 1670
Db 1487 /db 627 TTGTCGACTTAT 639

```

```

RESULT 6
BUS75069
DEFINITION PA_EA000918f Almond developing seed Prunus dulcis cDNA clone
ACCESSION BUS75069
VERSION BUS75069.1 GI:23031895
KEYWORDS EST
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis (almond)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids
Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 640)
Dandekar,A. Main.D., Wing,R. and Abbott,A.
Dept of Genetics and Biochemistry
1322 Union University, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 6879
Email: aabbert@clemson.edu
Web: www.clemson.edu/biochem
Seq primer: TATATGTCATCTATGAGG
High quality sequence stop: 640.
Location/Qualifiers
FEATURES

```

```

1. 640
/organism="Prunus dulcis"
/mot_type="mRNA"
/cutter="NdeI"
/clone="PA_EA000918f"
/tissue_type="embryo"
/lab_host="S. coli"
/development="developing seed"
/site="ECOR1, Site 2: XhoI;"
/synonym="Prunus amygdalus"
BASE COUNT 171 a 151 c 115 g 203 t
Quasi Match 18.3%; Score 394.6; DB 13; Length 640;
Best Local Similarity 82.1%; Pred. No. 4.4e-71;
Matches 454; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 1118 CAGATTTTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1177
Db 87 CAGATTTTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1178 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1237
Db 1176 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 1238 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1297
Db 1176 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 146
QY 207 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 266
Db 1298 AGCGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 326
QY 1297 TACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1297
Db 1298 AGCGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 326
QY 1358 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1417
Db 327 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 386
QY 1418 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1477
Db 387 ACATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 446
QY 1478 CACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 1537
Db 447 CACTCTCTGTCGAAGCTGCATTTTCAATCACTCAACCTTTAGTCTTTTCTCAAGACCT 506
QY 1538 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 1597
Db 507 TTTGTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 626
QY 1598 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 566
Db 567 ATGATTCAGATTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 626
QY 1658 TTGTCGACTTAT 1670
Db 627 TTGTCGACTTAT 639

```


AUTHORS **JOURNAL** **COMMENT**

Dandekar, A., Main, D., Wing, R., and Abbott, A.
Development of a Functional Genomics Database for Peach
Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
Clemson, SC 29634, USA
Tel: 864 656 1050
Fax: 864 656 6879
Email: aabert@clemson.edu
Fossil High Quality Bases = 634
Fossil High Quality Stop = 659.
High quality sequence stop = 659.

FEATURES **SOURCE**

1. 658
/db_xref="taxon:3755"
/clone_lib="Almond developing seed"
/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XbaI;
synonym: Prunus amygdalus"
Location/Qualifiers
1. 658 456 c 120 g 203 c

BASE COUNT **ORIGIN**

Query Match
Best Local Similarity 81.4%; DB 13; Length 658;
Matches 452; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1118 GAAATTCGACATTCGGAGTCATATATACGATCTCTGAGAACTCTCATAGCAT 1177
Db GAGGTTGACATCAGAGAGTCATATATACGATCTCTGAGAACTCTCATAGCAT 1177

Qy 1178 TTTTACCGGTATACGAGAGATTTATGTATGTCAGGCAATCGAAGCCTCAGCTTC 1237
Db GAGGTTGACATCAGAGAGTCATATATACGATCTCTGAGAACTCTCATAGCAT 1177

Qy 167 TTTTACCGGTATACGAGAGATTTATGTATGTCAGGCAATCGAAGCCTCAGCTTC 226
Db GAGGTTGACATCAGAGAGTCATATATACGATCTCTGAGAACTCTCATAGCAT 1177

Qy 1238 TACTATCTAGTGGGTGTCAGAGCTTACTACTCTCTGTCATGATCAGATGCTTC 1297
Db TACTATCTAGTGGGTGTCAGAGCTTACTACTCTCTGTCATGATCAGATGCTTC 1297

Qy 227 TACTATCTAGTGGGTGTCAGAGCTTACTACTCTCTGTCATGATCAGATGCTTC 286
Db TACTATCTAGTGGGTGTCAGAGCTTACTACTCTCTGTCATGATCAGATGCTTC 1297

Qy 1298 ACCCAATCTATGTGGCGAGTGTGTGATGATCATCTCTGATTAATCATTAATTT 1357
Db ACCCAATCTATGTGGCGAGTGTGTGATGATCATCTCTGATTAATCATTAATTT 1357

Qy 287 TTTTACCGGTATACGAGAGATTTATGTATGTCAGGCAATCGAAGCCTCAGCTTC 346
Db GAGGTTGACATCAGAGAGTCATATATACGATCTCTGAGAACTCTCATAGCAT 1177

Qy 1358 TGGCCCAATCAATCGATGATCTGTGTGATCTGTGTATGAGATAGAGATTAAT 1417
Db TGGCCCAATCAATCGATGATCTGTGTGATCTGTGTATGAGATAGAGATTAAT 1417

Qy 347 TGGCCCAATCAATCGATGATCTGTGTGATCTGTGTATGAGATAGAGATTAAT 406
Db TGGCCCAATCAATCGATGATCTGTGTGATCTGTGTATGAGATAGAGATTAAT 1417

Qy 1418 ATGAGTGTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1477
Db ATGAGTGTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1477

Qy 407 ACCAATCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 466
Db ACCAATCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1477

Qy 1478 CATCTACCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1537
Db CATCTACCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1478

Qy 467 CATCTACCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 526
Db CATCTACCTCTCTGAGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1478

Qy 1538 TGTTCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1597
Db TGTTCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1538

Qy 527 TATCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 586
Db TATCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1538

Qy 1598 ATTCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1657
Db ATTCATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1598

Qy 587 ATTTATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 646
Db ATTTATGCTGTCATGCTGTCATTTTCTGATCCTCAGCTTATGCTTCTGAGAA 1598

Qy 1658 TTGGTGACTTAT 1669
Db TTGGTGACTTAT 1658

RESULT 7 **LOCUS**

BU645516

DESCRIPTION

Almond cDNA library, Prunus dulcis cDNA 5' similar to

mandarionitrile lyase, mRNA sequence.

BU645516

ACCESSION

BU645516.1 GI:30271383

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS

PRUNUS DULCIS


```

RESULT 13
BUS74379
LOCUS BUS74379
DEFINITION BUS74379 622 bp mRNA linear EST 17-SEP-2002
PA_Ea0007DL17F Almond developing seed Prunus dulcis cDNA clone
ACCESSION PA_Ea0007DL17F, mRNA sequence.
VERSION BUS74379.1 GI:23031204
KEYWORDS EST.
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis (almond)
REFERENCE Ekmaroyka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids
; eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
AUTHORS Dandekar A., Main D., Wing R. and Abbott A.
TITLE Development of a Functional Genomics Database for Peach
JOURNAL Unpublished
COMMENT Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 4060
Email: aabbott@clemson.edu
Total High Quality bases = 600
Seq primer: TAATACGCTCACTATAGG
High quality sequence stop: 622.
FEATURES
SOURCE
1. 6220
/organism="Prunus dulcis"
/mol_type="mRNA"
/db_xref="taxon:3755"
/db_xref="taxon:3755"
/clone="PA_Ea0007DL17F"
/tissue_type="embryo"
/lab_host="E. coli"
/notes="developing seed"
/synonym="Prunus amygdalus"
BASE COUNT 169 a 141 c 134 g 178 t
ORIGIN
Query Match 11.2%; Score 242.6; DB 13; Length 622;
Best Local Similarity 84.7%; Pred. No. 1.2e-39;
Matches 272; Conservative 49; Mismatches 49; Indels 0; Gaps 0;
Qy 283 CACTGATACACCTCGAGAGATCATATGATATGATGATGAGAGACATCGG 348
Db 2 CAGGATCTAGGCTGGAGATCATATGATATGATGATGAGAGACATCGG 61
Qy 349 GTGTCATGCGACACATCTTACGAAAATACACAGCTGCTCTTCGAAAGGGAC 406
Db 62 GTGTCATGCGACACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 121
Qy 409 TCTGTCATGCGACACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 468
Db 122 TCTGTCATGCGACACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 468
Qy 469 ACAGATGATGAGAGACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 528
Db 182 ACAGATGATGAGAGACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 528
Qy 528 ACAGATGATGAGAGACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 588
Db 242 ACAGATGATGAGAGACATCTTACGAAAATACAGAGTCTCTTCGAAAGGGAC 588
Qy 589 ATTCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 609
Db 302 CACTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 622

```

```

RESULT 14
BUS72781
LOCUS BUS72781
DEFINITION BUS72781 543 bp mRNA linear EST 17-SEP-2002
PA_Ea0001014f Almond developing seed Prunus dulcis cDNA clone
ACCESSION BUS72781
VERSION BUS72781.1 GI:23031361
KEYWORDS EST.
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis (almond)
REFERENCE Ekmaroyka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids
; eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
AUTHORS Dandekar A., Main D., Wing R. and Abbott A.
TITLE Development of a Functional Genomics Database for Peach
JOURNAL Unpublished
COMMENT Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 4060
Email: aabbott@clemson.edu
Total High Quality bases = 531
Seq primer: TAATACGCTCACTATAGG
High quality sequence stop: 543.
FEATURES
SOURCE
1. 543
/organism="Prunus dulcis"
/mol_type="mRNA"
/db_xref="taxon:3755"
/db_xref="taxon:3755"
/clone="PA_Ea0001014f"
/tissue_type="embryo"
/lab_host="E. coli"
/notes="developing seed"
/synonym="Prunus amygdalus"
BASE COUNT 166 a 106 c 111 g 158 t
ORIGIN
Query Match 8.6%; Score 185.4; DB 13; Length 543;
Best Local Similarity 71.7%; Pred. No. 7.6e-26;
Matches 240; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
Qy 1720 GACGCTTTTCATTATTTGGAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 1779
Db 3 GAGGCTTTTCATTATTTGGAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 62
Qy 1780 GAAACATTTTGTCTAGATATATAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 182
Db 63 GAAACATTTTGTCTAGATATATAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 122
Qy 1840 GCGAAGTCTCTAGATATATAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 1859
Db 123 GCGAAGTCTCTAGATATATAGTCTCTTCCAGAGAACCAAGATGATGATCTTC 182
Qy 1900 GCCTTCATCTTCCAGAGAACCAAGATGATGATCTTCAGAGTCTTCAGT 1959
Db 183 GCCTTCATCTTCCAGAGAACCAAGATGATGATCTTCAGAGTCTTCAGT 242
Qy 1960 AGCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2019
Db 243 AGCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2019
Qy 2020 GAACTCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCATCT 2058
Db 303 TCCCTAGTCCAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 341

```

```

RESULT 15
B0106017

```

Search completed: December 18, 2003, 18:44:38
Job time : 4540 secs

Db 1381 TCTGTGTGACGTTTGTAGGCTTATAGAGGCTATATATATATAGTTTCTGTCTGACGTTG 1440
 Qy 1441 CAATTTTCCATCCACCTCTAGTCTTTTCTCAGACATCTATACCTCCCAACATTCG 1500
 Db 1441 CAATTTTCCATCCACCTCTAGTCTTTTCTCAGACATCTATACCTCCCAACATTCG 1500
 Qy 1501 ACTTTTGTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1560
 Db 1501 ACTTTTGTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1560
 Qy 1561 AATCTCATCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1620
 Db 1561 AATCTCATCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1620
 Qy 1621 AAGCACTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1680
 Db 1621 AAGCACTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1680
 Qy 1681 GCAATGAGCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1740
 Db 1681 GCAATGAGCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1740
 Qy 1741 GTAATCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1800
 Db 1741 GTAATCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1800
 Qy 1801 GTATCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1860
 Db 1801 GTATCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1860
 Qy 1861 TTCCTGTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1920
 Db 1861 TTCCTGTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1920
 Qy 1921 TCGAAGCACTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1980
 Db 1921 TCGAAGCACTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 1980
 Qy 1981 AACCACTGAGATCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 2040
 Db 1981 AACCACTGAGATCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 2040
 Qy 2041 TTTTCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 2100
 Db 2041 TTTTCTCTCTCATCTCTAGCAAGTTCAGAGCACTGTCTCTAGTGTCTGTACAGCTTA 2100
 Qy 2101 AAGAGAGTCAATCTCTGAGGCTTATCTATATATATATATATATATATATATATATATAT 2160
 Db 2101 AAGAGAGTCAATCTCTGAGGCTTATCTATATATATATATATATATATATATATATATAT 2160
 Qy 2161 CG 2162
 Db 2161 CG 2162

RESULT 2

AAFF8779

ID AAFF8779 standard; DNA; 1632 BP.

XX AC

XX AC

XX AAFF8779;

DT 11-DEC-2002 (first entry)

XX *P. amygdalius/h. niger* HNU5/fox fusion construct PAMHNU5xGDX DNA.
 XX Almond; hydroxynitrile lyase; HNU5; (R)-cyanohydrin synthetase; vitamin;
 KW (S)-cyanohydrin synthetase; pyrethroid; gene; fusion construct;
 XX glucose oxidase; de.
 OS Chimeric - *Prunus amygdalius*.
 OS Chimeric - *Aspergillus niger*.
 OS Synthetic.

XX Key
 PH CDS
 XX 10..1614
 XX /product= "HNU5/glucose oxidase fusion construct"
 XX
 XX EPI1232320-Al.
 XX 17-JUL-2002.
 XX
 XX 18-DEC-2001; 2001EP-0130058.
 XX 15-JUN-2001; 2001AT-0000060.
 XX 03-APR-2001; 2001AT-0000523.
 XX
 XX (STM) DSM FINE CHEM AUSTRIA NFG GMBH & CO KG.
 XX Schwab H, Glieder A, Kratky C, Drevovsky I, Pochlauer P, Stranc W;
 XX Mayrhofer H, Wirth I, Neuhof R, Bona R;
 XX P-PSUB; AAB14195.
 XX
 XX NPI 2002-445697/70.
 XX
 XX New gene for hydroxynitrile lyase from *Prunus* species, useful for
 XX stereospecific synthesis of cyanohydrin -
 XX
 XX Example 10; Fig 3; 49pp; German.
 XX
 XX This invention describes a novel gene that encodes a hydroxynitrile lyase
 XX (HNU) isolated using one PCR primer based on the 5'-region of the mdl
 XX gene from *Prunus amygdalius* and another primer based on the 3'-region
 XX of the 3'-region of an HNU isoenzyme from the same species. The signal
 XX region of the HNU protein can be used for secretory expression of
 XX heterologous proteins, e.g. fusion proteins, with HNU activity in host
 XX cells. The function of the HNU protein is useful for synthesis of (R)- or
 XX (S)-cyanohydrins, e.g. for pyrethroid synthesis. The signal region
 XX of the HNU protein is useful for synthesis of (R)- or (S)-pyrethroids.
 XX amounts of HNU, and these allow stereoselective synthesis of both (R)-
 XX (S)-cyanohydrins. This sequence encodes a fusion construct containing
 XX the HNU protein and a glucose oxidase (GOx) protein described in the method of the invention.

XX Sequence 1632 BP; 451 A; 357 C; 361 G; 463 T; 0 other;

Query Match

Best Local Similarity 58.8%; Score 1272; DB 24; Length 1632;

Matches 1489; Conservative 0; Mismatches 0; Indels 203; Gaps 1;

Qy 281 TACACGCCACTATACAGCTCTGAGAGCTATATATATATATATATATATATATATATATAT 1;
 Db 94 TACACGCCACTATACAGCTCTGAGAGCTATATATATATATATATATATATATATATAT 153

Qy 341 ACATCAGGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 400
 Db 154 ACATCAGGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 213

Qy 401 AAGGCGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 400
 Db 214 AAGGCGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 213

Qy 461 CTGACGACAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 520
 Db 274 CTGACGACAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 333

Qy 520 GATATATGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 580
 Db 334 GATATATGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 393

Qy 581 AGACCTAACCTCTCTATATAGTCAACAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 640
 Db 394 AGACCTAACCTCTCTATATAGTCAACAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 453

Qy 641 GAGATATATGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTG 700

Db 454 AAGACATATGATGGATGAGAGAGCCATTTGGGTGACAGCCAAATATCAATTTGGCAA 513
 Qy 701 TCTGTATAGAGAGAGATCTCTGACAGCGGTATCTCTGAGAGATGAGATGATTTG 760
 Db 514 TCTGTATAGAGAGAGATCTCTGAGAGCGGTATCTCTGAGAGATGAGATGATTTG 573
 Qy 761 GATCACTAGAGAGAGATCTCTGAGAGCGGTATCTCTGAGAGATGAGATGATTTG 830
 Db 574 GATCACTAGAGAGAGATCTCTGAGAGCGGTATCTCTGAGAGATGAGATGATTTG 623
 Qy 821 CGCGGTATGAGATCTCTGAGAGCGGTATCTCTGAGAGATGAGATGATTTG 880
 Db 634 CGCGGTATGAGATCTCTGAGAGCGGTATCTCTGAGAGATGAGATGATTTG 693
 Qy 881 TCGATAGAGAGATCT 940
 Db 694 TCGATAGAGAGATCT 730
 Qy 941 ATGTGTAGCT 1000
 Db 731 ----- 730
 Qy 1001 CTAGAGATGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1060
 Db 731 ----- 730
 Qy 1061 AATCTTCCAAATCT 1120
 Db 731 ----- 730
 Qy 1121 ATTGTGAGCTATGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1180
 Db 731 ATTGTGAGCTATGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 790
 Qy 1181 TAGCGGTATGAGAGATGATTTGTTAGTGCAGGCAATCGAGCCCTCAAGCTTAC 1240
 Db 791 TAGCGGTATGAGAGATGATTTGTTAGTGCAGGCAATCGAGCCCTCAAGCTTAC 850
 Qy 1241 TACTTATGTCGTGAGAGAGATGATTTGTTAGTGCAGGCAATCGAGCCCTCAAGCT 1300
 Db 851 TACTTATGTCGTGAGAGAGATGATTTGTTAGTGCAGGCAATCGAGCCCTCAAGCT 910
 Qy 1301 CGATCT 1360
 Db 911 CGATCT 970
 Qy 1361 CCCCAATCCATATGAGCT 1420
 Db 971 CCCCAATCCATATGAGCT 1030
 Qy 1421 ATGTTCT 1480
 Db 1031 ATGTTCT 1090
 Qy 1481 CTAGAGATGATGATGATCT 1540
 Db 1091 CTAGAGATGATGATGATCT 1150
 Qy 1541 CTAGAGATGATGATGATCT 1600
 Db 1151 CTAGAGATGATGATGATCT 1210
 Qy 1601 TCGATAGAGAGATCT 1660
 Db 1211 TCGATAGAGAGATCT 1270
 Qy 1661 CTGATCTTATAGAGAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1720
 Db 1271 CTGATCTTATAGAGAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1330
 Qy 1721 AGCTTTCT 1780

Db 1331 ACGTTTCTCAATATTGGAGTACTTTGTCAGAGAGCAACAGCAGTGCATCTCTCG 1390
 Qy 1781 AATCTTTCTAGATTAATGACTTTATCTGGATATCACTCGAGAGACCTTTGTTG 1840
 Db 1391 AATCTTTCTAGATTAATGACTTTATCTGGATATCACTCGAGAGACCTTTGTTG 1450
 Qy 1841 GGAATCTCTGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1900
 Db 1451 GGAATCTCTGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1510
 Qy 1901 CTCTCACTTTCT 1960
 Db 1511 CTCTCACTTTCT 1570
 Qy 1961 GGTATGTTG 1968
 Db 1571 GGTATGTTG 1578
 RESULT 3
 AAF88780 AAF88780 standard; DNA, 2087 bp.
 XX AAF88780;
 AC 11-DEC-2002 (first entry)
 XX 11-DEC-2002 (first entry)
 DE Almond HML1 DNA fragment.
 XX
 XX Almond; hydroxymethylase; HML; (R)-cyanohydrin synthesis; vitamin;
 XX (S)-cyanohydrin synthesis; pyrenoid; gene; de.
 OS Prunus amygdalus.
 XX Key
 XX CDS
 location/Qualifiers
 1..2087
 /tag= a
 /product= "HML1"
 /note= "partial CDS with no stop codon. CDS is
 interrupted by introns"
 exon 1..103
 /tag= b
 /numbers= 1
 /start= 1
 /end= 249
 /tag= c
 /numbers= 1
 /start= 250
 /end= 906
 /tag= d
 /numbers= 2
 /start= 907
 /end= 1047
 /tag= e
 /numbers= 2
 /start= 1048
 /end= 1188
 /tag= f
 /numbers= 3
 /start= 1189
 /end= 1993
 /tag= g
 /numbers= 3
 /start= 1994
 /end= 2087
 /tag= h
 /numbers= 4
 /note= "partial, no stop codon given"
 EP12323220-1.
 17-JUL-2002.
 18-DEC-2001; 2001EP-0130058.
 16-JAN-2001; 2001AT-0000060.
 03-APR-2001; 2001AT-0000523.
 (STAM) DSM FINE CHEM AUSTRIA NFG GMBH & CO. KG.

KW Hybridization assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 KW *Arabidopsis thaliana*.

XX EPI033405-A2.
 XX
 XX 06-SEP-2000.
 XX
 XX
 XX
 XX 25-FEB-2000; 2000SEP-0301439.
 XX 25-FEB-1999; 99US-0121855.
 XX 26-FEB-1999; 99US-0121856.
 XX 05-MAR-1999; 99US-0123598.
 XX 21-MAR-1999; 99US-0125788.
 XX 25-MAR-1999; 99US-0126264.
 XX 01-APR-1999; 99US-0127462.
 XX 06-APR-1999; 99US-0128234.
 XX 08-APR-1999; 99US-0128714.
 XX 15-APR-1999; 99US-0129077.
 XX 21-APR-1999; 99US-0130449.
 XX 23-APR-1999; 99US-0130510.
 XX 25-APR-1999; 99US-0130891.
 XX 28-APR-1999; 99US-0132048.
 XX 30-APR-1999; 99US-0132048.
 XX 30-APR-1999; 99US-0132407.
 XX 04-MAY-1999; 99US-0132484.
 XX 05-MAY-1999; 99US-0132486.
 XX 06-MAY-1999; 99US-0132487.
 XX 07-MAY-1999; 99US-0132863.
 XX 11-MAY-1999; 99US-0134256.
 XX 14-MAY-1999; 99US-0134256.
 XX 14-MAY-1999; 99US-0134219.
 XX 14-MAY-1999; 99US-0134221.
 XX 14-MAY-1999; 99US-0134370.
 XX 15-MAY-1999; 99US-0134941.
 XX 20-MAY-1999; 99US-0135124.
 XX 21-MAY-1999; 99US-0135353.
 XX 22-MAY-1999; 99US-0136021.
 XX 24-MAY-1999; 99US-0136392.
 XX 28-MAY-1999; 99US-0136782.
 XX 01-JUN-1999; 99US-0137222.
 XX 04-JUN-1999; 99US-0137502.
 XX 07-JUN-1999; 99US-0137724.
 XX 08-JUN-1999; 99US-0138094.
 XX 10-JUN-1999; 99US-0138847.
 XX 10-JUN-1999; 99US-0138847.
 XX 14-JUN-1999; 99US-0139119.
 XX 16-JUN-1999; 99US-0139452.
 XX 16-JUN-1999; 99US-0139453.
 XX 18-JUN-1999; 99US-0139454.
 XX 18-JUN-1999; 99US-0139454.
 XX 18-JUN-1999; 99US-0139455.
 XX 18-JUN-1999; 99US-0139456.
 XX 18-JUN-1999; 99US-0139456.
 XX 18-JUN-1999; 99US-0139459.
 XX 18-JUN-1999; 99US-0139459.
 XX 18-JUN-1999; 99US-0139460.
 XX 18-JUN-1999; 99US-0139461.
 XX 18-JUN-1999; 99US-0139463.
 XX 18-JUN-1999; 99US-0139463.
 XX 18-JUN-1999; 99US-0139750.
 XX 18-JUN-1999; 99US-0139763.
 XX 21-JUN-1999; 99US-0139817.
 XX 21-JUN-1999; 99US-0139817.
 XX 23-JUN-1999; 99US-0140353.
 XX 23-JUN-1999; 99US-0140354.
 XX 24-JUN-1999; 99US-0140823.
 XX 28-JUN-1999; 99US-0140991.
 XX 01-JUL-1999; 99US-0141844.
 XX 01-JUL-1999; 99US-0142154.
 XX 02-JUL-1999; 99US-0142055.
 XX 03-JUL-1999; 99US-0142055.
 XX 08-JUL-1999; 99US-0142805.
 XX 09-JUL-1999; 99US-0142920.
 XX 12-JUL-1999; 99US-0142977.
 XX 12-JUL-1999; 99US-0143542.
 XX 13-JUL-1999; 99US-0143542.
 XX 15-JUL-1999; 99US-0144005.
 XX 16-JUL-1999; 99US-0144085.
 XX 16-JUL-1999; 99US-0144086.
 XX 16-JUL-1999; 99US-0144086.
 XX 19-JUL-1999; 99US-0144331.
 XX 19-JUL-1999; 99US-0144332.
 XX 19-JUL-1999; 99US-0144333.
 XX 19-JUL-1999; 99US-0144333.
 XX 19-JUL-1999; 99US-0144335.
 XX 20-JUL-1999; 99US-0144352.
 XX 20-JUL-1999; 99US-0144352.
 XX 20-JUL-1999; 99US-0144884.
 XX 21-JUL-1999; 99US-0145086.
 XX 21-JUL-1999; 99US-0145088.
 XX 22-JUL-1999; 99US-0145085.
 XX 22-JUL-1999; 99US-0145085.
 XX 22-JUL-1999; 99US-0145089.
 XX 22-JUL-1999; 99US-0145192.
 XX 23-JUL-1999; 99US-0145145.
 XX 23-JUL-1999; 99US-0145218.
 XX 24-JUL-1999; 99US-0145218.
 XX 26-JUL-1999; 99US-0145276.
 XX 27-JUL-1999; 99US-0145913.
 XX 27-JUL-1999; 99US-0145918.
 XX 27-JUL-1999; 99US-0145918.
 XX 28-JUL-1999; 99US-0145951.
 XX 02-AUG-1999; 99US-0146386.
 XX 02-AUG-1999; 99US-0146388.
 XX 02-AUG-1999; 99US-0146389.
 XX 02-AUG-1999; 99US-0146389.
 XX 04-AUG-1999; 99US-0147204.
 XX 04-AUG-1999; 99US-0147302.
 XX 05-AUG-1999; 99US-0147302.
 XX 05-AUG-1999; 99US-0147302.
 XX 06-AUG-1999; 99US-0147303.
 XX 06-AUG-1999; 99US-0147416.
 XX 09-AUG-1999; 99US-0147493.
 XX 09-AUG-1999; 99US-0147493.
 XX 09-AUG-1999; 99US-0147493.
 XX 11-AUG-1999; 99US-0148319.
 XX 12-AUG-1999; 99US-0148341.
 XX 13-AUG-1999; 99US-0148565.
 XX 13-AUG-1999; 99US-0148565.
 XX 16-AUG-1999; 99US-0148568.
 XX 17-AUG-1999; 99US-0149175.
 XX 18-AUG-1999; 99US-0149426.
 XX 20-AUG-1999; 99US-0149722.
 XX 20-AUG-1999; 99US-0149722.
 XX 20-AUG-1999; 99US-0149929.
 XX 23-AUG-1999; 99US-0149902.
 XX 23-AUG-1999; 99US-0149930.
 XX 23-AUG-1999; 99US-0149930.
 XX 25-AUG-1999; 99US-0150684.
 XX 25-AUG-1999; 99US-0150684.
 XX 27-AUG-1999; 99US-0151085.
 XX 27-AUG-1999; 99US-0151086.
 XX 27-AUG-1999; 99US-0151086.
 XX 27-AUG-1999; 99US-0151086.
 XX 31-AUG-1999; 99US-0151438.

Qy 794 ACTTTTCGAATATGAGACGGCATCGCGCTGATGAATCTCTTATAAGGAGACCT 853
 Dd ATTTTTCGAATATGAGACGGCATCGCGCTGATGAATCTCTTATAAGGAGACCT 719
 Qy 854 AATACTCTGCTAGTTCAGAGTTCAGAGCTCTCAGTAGAGAGATCTCTT 900
 Dd AGGATATACGCTTCTTTCATGATCCACCTCCACCGGATCTTCTT 766

RESULT 8

ACAC40757
 XX ACAC40757 standard; DNA, 2098 BP.
 AC AAC40757;
 XX
 XX 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29440.
 DE
 XX Hybridization assay; genetic mapping, gene expression control;
 KW Arabidopsis thaliana; Arabidopsis thaliana; Arabidopsis thaliana;
 KW metabolic pathway; promoter; termination sequence; ss.
 KW
 QS Arabidopsis thaliana.
 PK
 PK EP1033405-A2.
 PK
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 XX

PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 15-MAR-1999; 99US-0123180.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 25-MAR-1999; 99US-0126785.
 PR 04-APR-1999; 99US-0128231.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 21-APR-1999; 99US-0130077.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 05-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132863.
 PR 07-MAY-1999; 99US-0132865.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 20-MAY-1999; 99US-0134911.
 PR 20-MAY-1999; 99US-0135353.
 PR 21-MAY-1999; 99US-0135629.
 PR 24-MAY-1999; 99US-0136021.
 PR 25-MAY-1999; 99US-0136021.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 04-JUN-1999; 99US-0138094.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138647.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 17-JUN-1999; 99US-0139452.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 22-JUN-1999; 99US-0139859.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141314.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142350.
 PR 08-JUL-1999; 99US-0142603.
 PR 12-JUL-1999; 99US-0142603.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0143624.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144684.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 23-JUL-1999; 99US-0145114.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 23-JUL-1999; 99US-0145224.
 PR 23-JUL-1999; 99US-0145224.
 PR 23-JUL-1999; 99US-0145224.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147303.
 PR 09-AUG-1999; 99US-0147431.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.

```

PR 11-AUG-1999/ 99US-0148119.
PR 12-AUG-1999/ 99US-0148341.
PR 13-AUG-1999/ 99US-0148561.
PR 14-AUG-1999/ 99US-0148781.
PR 15-AUG-1999/ 99US-0149001.
PR 16-AUG-1999/ 99US-0149261.
PR 17-AUG-1999/ 99US-0149478.
PR 18-AUG-1999/ 99US-0149698.
PR 19-AUG-1999/ 99US-0149918.
PR 20-AUG-1999/ 99US-0149722.
PR 21-AUG-1999/ 99US-0149942.
PR 22-AUG-1999/ 99US-0149962.
PR 23-AUG-1999/ 99US-0149982.
PR 24-AUG-1999/ 99US-0150002.
PR 25-AUG-1999/ 99US-0150220.
PR 26-AUG-1999/ 99US-0150438.
PR 27-AUG-1999/ 99US-0150656.
PR 28-AUG-1999/ 99US-0150874.
PR 29-AUG-1999/ 99US-0151092.
PR 30-AUG-1999/ 99US-0151310.
PR 31-AUG-1999/ 99US-0151528.
PR 01-SEP-1999/ 99US-0151746.
PR 02-SEP-1999/ 99US-0151964.
PR 03-SEP-1999/ 99US-0152182.
PR 04-SEP-1999/ 99US-0152400.
PR 05-SEP-1999/ 99US-0152618.
PR 06-SEP-1999/ 99US-0152836.
PR 07-SEP-1999/ 99US-0153054.
PR 08-SEP-1999/ 99US-0153272.
PR 09-SEP-1999/ 99US-0153490.
PR 10-SEP-1999/ 99US-0153708.
PR 11-SEP-1999/ 99US-0153926.
PR 12-SEP-1999/ 99US-0154144.
PR 13-SEP-1999/ 99US-0154362.
PR 14-SEP-1999/ 99US-0154580.
PR 15-SEP-1999/ 99US-0154798.
PR 16-SEP-1999/ 99US-0155016.
PR 17-SEP-1999/ 99US-0155234.
PR 18-SEP-1999/ 99US-0155452.
PR 19-SEP-1999/ 99US-0155670.
PR 20-SEP-1999/ 99US-0155888.
PR 21-SEP-1999/ 99US-0156106.
PR 22-SEP-1999/ 99US-0156324.
PR 23-SEP-1999/ 99US-0156542.
PR 24-SEP-1999/ 99US-0156760.
PR 25-SEP-1999/ 99US-0156978.
PR 26-SEP-1999/ 99US-0157196.
PR 27-SEP-1999/ 99US-0157414.
PR 28-SEP-1999/ 99US-0157632.
PR 29-SEP-1999/ 99US-0157850.
PR 30-SEP-1999/ 99US-0158068.
PR 01-OCT-1999/ 99US-0158286.
PR 02-OCT-1999/ 99US-0158504.
PR 03-OCT-1999/ 99US-0158722.
PR 04-OCT-1999/ 99US-0158940.
PR 05-OCT-1999/ 99US-0159158.
PR 06-OCT-1999/ 99US-0159376.
PR 07-OCT-1999/ 99US-0159594.
PR 08-OCT-1999/ 99US-0159812.
PR 09-OCT-1999/ 99US-0159999.
PR 10-OCT-1999/ 99US-0160217.
PR 11-OCT-1999/ 99US-0160435.
PR 12-OCT-1999/ 99US-0160653.
PR 13-OCT-1999/ 99US-0160871.
PR 14-OCT-1999/ 99US-0161089.
PR 15-OCT-1999/ 99US-0161307.
PR 16-OCT-1999/ 99US-0161525.
PR 17-OCT-1999/ 99US-0161743.
PR 18-OCT-1999/ 99US-0161961.
PR 19-OCT-1999/ 99US-0162179.
PR 20-OCT-1999/ 99US-0162397.
PR 21-OCT-1999/ 99US-0162615.
PR 22-OCT-1999/ 99US-0162833.
PR 23-OCT-1999/ 99US-0163051.
PR 24-OCT-1999/ 99US-0163269.
PR 25-OCT-1999/ 99US-0163487.
PR 26-OCT-1999/ 99US-0163705.
PR 27-OCT-1999/ 99US-0163923.
PR 28-OCT-1999/ 99US-0164141.
PR 29-OCT-1999/ 99US-0164359.
PR 30-OCT-1999/ 99US-0164577.
PR 31-OCT-1999/ 99US-0164795.
PR 01-NOV-1999/ 99US-0165013.
PR 02-NOV-1999/ 99US-0165231.
PR 03-NOV-1999/ 99US-0165449.
PR 04-NOV-1999/ 99US-0165667.
PR 05-NOV-1999/ 99US-0165885.
PR 06-NOV-1999/ 99US-0166103.
PR 07-NOV-1999/ 99US-0166321.
PR 08-NOV-1999/ 99US-0166539.
PR 09-NOV-1999/ 99US-0166757.
PR 10-NOV-1999/ 99US-0166975.
PR 11-NOV-1999/ 99US-0167193.
PR 12-NOV-1999/ 99US-0167411.
PR 13-NOV-1999/ 99US-0167629.
PR 14-NOV-1999/ 99US-0167847.
PR 15-NOV-1999/ 99US-0168065.
PR 16-NOV-1999/ 99US-0168283.
PR 17-NOV-1999/ 99US-0168501.
PR 18-NOV-1999/ 99US-0168719.
PR 19-NOV-1999/ 99US-0168937.
PR 20-NOV-1999/ 99US-0169155.
PR 21-NOV-1999/ 99US-0169373.
PR 22-NOV-1999/ 99US-0169591.
PR 23-NOV-1999/ 99US-0169809.
PR 24-NOV-1999/ 99US-0170027.
PR 25-NOV-1999/ 99US-0170245.
PR 26-NOV-1999/ 99US-0170463.
PR 27-NOV-1999/ 99US-0170681.
PR 28-NOV-1999/ 99US-0170899.
PR 29-NOV-1999/ 99US-0171117.
PR 30-NOV-1999/ 99US-0171335.
PR 01-DEC-1999/ 99US-0171553.
PR 02-DEC-1999/ 99US-0171771.
PR 03-DEC-1999/ 99US-0171989.
PR 04-DEC-1999/ 99US-0172207.
PR 05-DEC-1999/ 99US-0172425.
PR 06-DEC-1999/ 99US-0172643.
PR 07-DEC-1999/ 99US-0172861.
PR 08-DEC-1999/ 99US-0173079.
PR 09-DEC-1999/ 99US-0173297.
PR 10-DEC-1999/ 99US-0173515.
PR 11-DEC-1999/ 99US-0173733.
PR 12-DEC-1999/ 99US-0173951.
PR 13-DEC-1999/ 99US-0174169.
PR 14-DEC-1999/ 99US-0174387.
PR 15-DEC-1999/ 99US-0174605.
PR 16-DEC-1999/ 99US-0174823.
PR 17-DEC-1999/ 99US-0175041.
PR 18-DEC-1999/ 99US-0175259.
PR 19-DEC-1999/ 99US-0175477.
PR 20-DEC-1999/ 99US-0175695.
PR 21-DEC-1999/ 99US-0175913.
PR 22-DEC-1999/ 99US-0176131.
PR 23-DEC-1999/ 99US-0176349.
PR 24-DEC-1999/ 99US-0176567.
PR 25-DEC-1999/ 99US-0176785.
PR 26-DEC-1999/ 99US-0177003.
PR 27-DEC-1999/ 99US-0177221.
PR 28-DEC-1999/ 99US-0177439.
PR 29-DEC-1999/ 99US-0177657.
PR 30-DEC-1999/ 99US-0177875.
PR 31-DEC-1999/ 99US-0178093.
PR 01-JAN-2000/ 99US-0178311.
PR 02-JAN-2000/ 99US-0178529.
PR 03-JAN-2000/ 99US-0178747.
PR 04-JAN-2000/ 99US-0178965.
PR 05-JAN-2000/ 99US-0179183.
PR 06-JAN-2000/ 99US-0179401.
PR 07-JAN-2000/ 99US-0179619.
PR 08-JAN-2000/ 99US-0179837.
PR 09-JAN-2000/ 99US-0180055.
PR 10-JAN-2000/ 99US-0180273.
PR 11-JAN-2000/ 99US-0180491.
PR 12-JAN-2000/ 99US-0180709.
PR 13-JAN-2000/ 99US-0180927.
PR 14-JAN-2000/ 99US-0181145.
PR 15-JAN-2000/ 99US-0181363.
PR 16-JAN-2000/ 99US-0181581.
PR 17-JAN-2000/ 99US-0181799.
PR 18-JAN-2000/ 99US-0182017.
PR 19-JAN-2000/ 99US-0182235.
PR 20-JAN-2000/ 99US-0182453.
PR 21-JAN-2000/ 99US-0182671.
PR 22-JAN-2000/ 99US-0182889.
PR 23-JAN-2000/ 99US-0183107.
PR 24-JAN-2000/ 99US-0183325.
PR 25-JAN-2000/ 99US-0183543.
PR 26-JAN-2000/ 99US-0183761.
PR 27-JAN-2000/ 99US-0183979.
PR 28-JAN-2000/ 99US-0184197.
PR 29-JAN-2000/ 99US-0184415.
PR 30-JAN-2000/ 99US-0184633.
PR 31-JAN-2000/ 99US-0184851.
PR 01-FEB-2000/ 99US-0185069.
PR 02-FEB-2000/ 99US-0185287.
PR 03-FEB-2000/ 99US-0185505.
PR 04-FEB-2000/ 99US-0185723.
PR 05-FEB-2000/ 99US-0185941.
PR 06-FEB-2000/ 99US-0186159.
PR 07-FEB-2000/ 99US-0186377.
PR 08-FEB-2000/ 99US-0186595.
PR 09-FEB-2000/ 99US-0186813.
PR 10-FEB-2000/ 99US-0187031.
PR 11-FEB-2000/ 99US-0187249.
PR 12-FEB-2000/ 99US-0187467.
PR 13-FEB-2000/ 99US-0187685.
PR 14-FEB-2000/ 99US-0187903.
PR 15-FEB-2000/ 99US-0188121.
PR 16-FEB-2000/ 99US-0188339.
PR 17-FEB-2000/ 99US-0188557.
PR 18-FEB-2000/ 99US-0188775.
PR 19-FEB-2000/ 99US-0188993.
PR 20-FEB-2000/ 99US-0189211.
PR 21-FEB-2000/ 99US-0189429.
PR 22-FEB-2000/ 99US-0189647.
PR 23-FEB-2000/ 99US-0189865.
PR 24-FEB-2000/ 99US-0190083.
PR 25-FEB-2000/ 99US-0190301.
PR 26-FEB-2000/ 99US-0190519.
PR 27-FEB-2000/ 99US-0190737.
PR 28-FEB-2000/ 99US-0190955.
PR 29-FEB-2000/ 99US-0191173.
PR 01-MAR-2000/ 99US-0191391.
PR 02-MAR-2000/ 99US-0191609.
PR 03-MAR-2000/ 99US-0191827.
PR 04-MAR-2000/ 99US-0192045.
PR 05-MAR-2000/ 99US-0192263.
PR 06-MAR-2000/ 99US-0192481.
PR 07-MAR-2000/ 99US-0192699.
PR 08-MAR-2000/ 99US-0192917.
PR 09-MAR-2000/ 99US-0193135.
PR 10-MAR-2000/ 99US-0193353.
PR 11-MAR-2000/ 99US-0193571.
PR 12-MAR-2000/ 99US-0193789.
PR 13-MAR-2000/ 99US-0194007.
PR 14-MAR-2000/ 99US-0194225.
PR 15-MAR-2000/ 99US-0194443.
PR 16-MAR-2000/ 99US-0194661.
PR 17-MAR-2000/ 99US-0194879.
PR 18-MAR-2000/ 99US-0195097.
PR 19-MAR-2000/ 99US-0195315.
PR 20-MAR-2000/ 99US-0195533.
PR 21-MAR-2000/ 99US-0195751.
PR 22-MAR-2000/ 99US-0195969.
PR 23-MAR-2000/ 99US-0196187.
PR 24-MAR-2000/ 99US-0196405.
PR 25-MAR-2000/ 99US-0196623.
PR 26-MAR-2000/ 99US-0196841.
PR 27-MAR-2000/ 99US-0197059.
PR 28-MAR-2000/ 99US-0197277.
PR 29-MAR-2000/ 99US-0197495.
PR 30-MAR-2000/ 99US-0197713.
PR 31-MAR-2000/ 99US-0197931.
PR 01-APR-2000/ 99US-0198149.
PR 02-APR-2000/ 99US-0198367.
PR 03-APR-2000/ 99US-0198585.
PR 04-APR-2000/ 99US-0198803.
PR 05-APR-2000/ 99US-0199021.
PR 06-APR-2000/ 99US-0199239.
PR 07-APR-2000/ 99US-0199457.
PR 08-APR-2000/ 99US-0199675.
PR 09-APR-2000/ 99US-0199893.
PR 10-APR-2000/ 99US-0200111.
PR 11-APR-2000/ 99US-0200329.
PR 12-APR-2000/ 99US-0200547.
PR 13-APR-2000/ 99US-0200765.
PR 14-APR-2000/ 99US-0200983.
PR 15-APR-2000/ 99US-0201201.
PR 16-APR-2000/ 99US-0201419.
PR 17-APR-2000/ 99US-0201637.
PR 18-APR-2000/ 99US-0201855.
PR 19-APR-2000/ 99US-0202073.
PR 20-APR-2000/ 99US-0202291.
PR 21-APR-2000/ 99US-0202509.
PR 22-APR-2000/ 99US-0202727.
PR 23-APR-2000/ 99US-0202945.
PR 24-APR-2000/ 99US-0203163.
PR 25-APR-2000/ 99US-0203381.
PR 26-APR-2000/ 99US-0203599.
PR 27-APR-2000/ 99US-0203817.
PR 28-APR-2000/ 99US-0204035.
PR 29-APR-2000/ 99US-0204253.
PR 30-APR-2000/ 99US-0204471.
PR 01-MAY-2000/ 99US-0204689.
PR 02-MAY-2000/ 99US-0204907.
PR 03-MAY-2000/ 99US-0205125.
PR 04-MAY-2000/ 99US-0205343.
PR 05-MAY-2000/ 99US-0205561.
PR 06-MAY-2000/ 99US-0205779.
PR 07-MAY-2000/ 99US-0205997.
PR 08-MAY-2000/ 99US-0206215.
PR 09-MAY-2000/ 99US-0206433.
PR 10-MAY-2000/ 99US-0206651.
PR 11-MAY-2000/ 99US-0206869.
PR 12-MAY-2000/ 99US-0207087.
PR 13-MAY-2000/ 99US-0207305.
PR 14-MAY-2000/ 99US-0207523.
PR 15-MAY-2000/ 99US-0207741.
PR 16-MAY-2000/ 99US-0207959.
PR 17-MAY-2000/ 99US-0208177.
PR 18-MAY-2000/ 99US-0208395.
PR 19-MAY-2000/ 99US-0208613.
PR 20-MAY-2000/ 99US-0208831.
PR 21-MAY-2000/ 99US-0209049.
PR 22-MAY-2000/ 99US-0209267.
PR 23-MAY-2000/ 99US-0209485.
PR 24-MAY-2000/ 99US-0209703.
PR 25-MAY-2000/ 99US-0209921.
PR 26-MAY-2000/ 99US-0210139.
PR 27-MAY-2000/ 99US-0210357.
PR 28-MAY-2000/ 99US-0210575.
PR 29-MAY-2000/ 99US-0210793.
PR 30-MAY-2000/ 99US-0211011.
PR 31-MAY-2000/ 99US-0211229.
PR 01-JUN-2000/ 99US-0211447.
PR 02-JUN-2000/ 99US-0211665.
PR 03-JUN-2000/ 99US-0211883.
PR 04-JUN-2000/ 99US-0212101.
PR 05-JUN-2000/ 99US-0212319.
PR 06-JUN-2000/ 99US-0212537.
PR 07-JUN-2000/ 99US-0212755.
PR 08-JUN-2000/ 99US-0212973.
PR 09-JUN-2000/ 99US-0213191.
PR 10-JUN-2000/ 99US-0213409.
PR 11-JUN-2000/ 99US-0213627.
PR 12-JUN-2000/ 99US-0213845.
PR 13-JUN-2000/ 99US-0214063.
PR 14-JUN-2000/ 99US-0214281.
PR 15-JUN-2000/ 99US-0214499.
PR 16-JUN-2000/ 99US-0214717.
PR 17-JUN-2000/ 99US-0214935.
PR 18-JUN-2000/ 99US-0215153.
PR 19-JUN-2000/ 99US-0215371.
PR 20-JUN-2000/ 99US-0215589.
PR 21-JUN-2000/ 99US-0215807.
PR 22-JUN-2000/ 99US-0216025.
PR 23-JUN-2000/ 99US-0216243.
PR 24-JUN-2000/ 99US-0216461.
PR 25-JUN-2000/ 99US-0216679.
PR 26-JUN-2000/ 99US-0216897.
PR 27-JUN-2000/ 99US-0217115.
PR 28-JUN-2000/ 99US-0217333.
PR 29-JUN-2000/ 99US-0217551.
PR 30-JUN-2000/ 99US-0217769.
PR 01-JUL-2000/ 99US-0217987.
PR 02-JUL-2000/ 99US-0218205.
PR 03-JUL-2000/ 99US-0218423.
PR 04-JUL-2000/ 99US-0218641.
PR 05-JUL-2000/ 99US-0218859.
PR 06-JUL-2000/ 99US-0219077.
PR 07-JUL-2000/ 99US-0219295.
PR 08-JUL-2000/ 99US-0219513.
PR 09-JUL-2000/ 99US-0219731.
PR 10-JUL-2000/ 99US-0219949.
PR 11-JUL-2000/ 99US-0220167.
PR 12-JUL-2000/ 99US-0220385.
PR 13-JUL-2000/ 99US-0220603.
PR 14-JUL-2000/ 99US-0220821.
PR 15-JUL-2000/ 99US-0221039.
PR 16-JUL-2000/ 99US-0221257.
PR 17-JUL-2000/ 99US-0221475.
PR 18-JUL-2000/ 99US-0221693.
PR 19-JUL-2000/ 99US-0221911.
PR 20-JUL-2000/ 99US-0222129.
PR 21-JUL-2000/ 99US-0222347.
PR 22-JUL-2000/ 99US-0222565.
PR 23-JUL-2000/ 99US-0222783.
PR 24-JUL-2000/ 99US-0223001.
PR 25-JUL-2000/ 99US-0223219.
PR 26-JUL-2000/ 99US-0223437.
PR 27-JUL-2000/ 99US-0223655.
PR 28-JUL-2000/ 99US-0223873.
PR 29-JUL-2000/ 99US-0224091.
PR 30-JUL-2000/ 99US-0224309.
PR 31-JUL-2000/ 99US-0224527.
PR 01-AUG-2000/ 99US-0224745.
PR 02-AUG-2000/ 99US-0224963.
PR 03-AUG-2000/ 99US-0225181.
PR 04-AUG-2000/ 99US-0225399.
PR 05-AUG-2000/ 99US-0225617.
PR 06-AUG-2000/ 99US-0225835.
PR 07-AUG-2000/ 99US-0226053.
PR 08-AUG-2000/ 99US-0226271.
PR 09-AUG-2000/ 99US-0226489.
PR 10-AUG-2000/ 99US-0226707.
PR 11-AUG-2000/ 99US-0226925.
PR 12-AUG-2000/ 99US-0227143.
PR 13-AUG-2000/ 99US-0227361.
PR 14-AUG-2000/ 99US-0227579.
PR 15-AUG-2000/ 99US-0227797.
PR 16-AUG-2000/ 99US-0228015.
PR 17-AUG-2000/ 99US-0228233.
PR 18-AUG-2000/ 99US-0228451.
PR 19-AUG-2000/ 99US-0228669.
PR 20-AUG-2000/ 99US-0228887.
PR 21-AUG-2000/ 99US-0229105.
PR 22-AUG-2000/ 99US-0229323.
PR 23-AUG-2000/ 99US-0229541.
PR 24-AUG-2000/ 99US-0229759.
PR 25-AUG-2000/ 99US-0229977.
PR 26-AUG-2000/ 99US-0230195.
PR 27-AUG-2000/ 99US-0230413.
PR 28-AUG-2000/ 99US-0230631.
PR 29-AUG-2000/ 99US-0230849.
PR 30-AUG-2000/ 99US-0231067.
PR 31-AUG-2000/ 99US-0231285.
PR 01-SEP-2000/ 99US-0231503.
PR 02-SEP-2000/ 99US-0231721.
PR 03-SEP-2000/ 99US-0231939.
PR 04-SEP-2000/ 99US-0232157.
PR 05-SEP-2000/ 99US-0232375.
PR 06-SEP-2000/ 99US-0232593.
PR 07-SEP-2000/ 99US-0232811.
PR 08-SEP-2000/ 99US-0233029.
PR 09-SEP-2000/ 99US-0233247.
PR 10-SEP-2000/ 99US-0233465.
PR 11-SEP-2000/ 99US-0233683.
PR 12-SEP-2000/ 99US-0233901.
PR 13-SEP-2000/ 99US-0234119.
PR 14-SEP-2000/ 99US-0234337.
PR 15-SEP-2000/ 99US-0234555.
PR 16-SEP-2000/ 99US-0234773.
PR 17-SEP-2000/ 99US-0234991.
PR 18-SEP-2000/ 99US-0235209.
PR 19-SEP-2000/ 99US-0235427.
PR 20-SEP-2000/ 99US-0235645.
PR 21-SEP-2000/ 99US-0235863.
PR 22-SEP-2000/ 99US-0236081.
PR 23-SEP-2000/ 99US-0236299.
PR 24-SEP-2000/ 99US-0236517.
PR 25-SEP-2000/ 99US-0236735.
PR 26-SEP-2000/ 99US-0236953.
PR 27-SEP-2000/ 99US-0237171.
PR 28-SEP-2000/ 99US-0237389.
PR 29-SEP-2000/ 99US-0237607.
PR 30-SEP-2000/ 99US-0237825.
PR 01-OCT-2000/ 99US-0238043.
PR 02-OCT-2000/ 99US-0238261.
PR 03-OCT-2000/ 99US-0238479.
PR 04-OCT-2000/ 99US-0238697.
PR 05-OCT-2000/ 99US-0238915.
PR 06-OCT-2000/ 99US-0239133.
PR 07-OCT-2000/ 99US-0239351.
PR 08-OCT-2000/ 99US-0239569.
PR 09-OCT-2000/ 99US-0239787.
PR 10-OCT-2000/ 99US-0240005.
PR 11-OCT-2000/ 99US-0240223.
PR 12-OCT-2000/ 99US-0240441.
PR 13-OCT-2000/ 99US-0240659.
PR 14-OCT-2000/ 99US-0240877.
PR 15-OCT-2000/ 99US-0241095.
PR 16-OCT-2000/ 99US-0241313.
PR 17-OCT-2000/ 99US-0241531.
PR 18-OCT-2000/ 99US-0241749.
PR 19-OCT-2000/ 99US-0241967.
PR 20-OCT-2000/ 99US-0242185.
PR 21-OCT-2000/ 99US-0242403.
PR 22-OCT-2000/ 99US-0242621.
PR 23-OCT-2000/ 99US-0242839.
PR 24-OCT-2000/ 99US-0243057.
PR 25-OCT-2000/ 99US-0243275.
PR 26-OCT-2000/ 99US-0243493.
PR 27-OCT-2000/ 99US-0243711.
PR 28-OCT-2000/ 99US-0243929.
PR 29-OCT-2000/ 99US-0244147.
PR 30-OCT-2000/ 99US-0244365.
PR 31-OCT-2000/ 99US-0244583.
PR 01-NOV-2000/ 99US-0244801.
PR 02-NOV-2000/ 99US-0245019.
PR 03-NOV-2000/ 99US-0245237.
PR 04-NOV-2000/ 99US-0245455.
PR 05-NOV-2000/ 99US-0245673.
PR 06-NOV-2000/ 99US-0245891.
PR 07-NOV-2000/ 99US-0246109.
PR 08-NOV-2000/ 99US-0246327.
PR 09-NOV-2000/ 99US-0246545.
PR 10-NOV-2000/ 99US-0246763.
PR 11-NOV-2000/ 99US-0246981.
PR 12-NOV-2000/ 99US-0247199.
PR 13-NOV-2000/ 99US-0247417.
PR 14-NOV-2000/ 99US-0247635.
PR 15-NOV-2000/ 99US-0247853.
PR 16-NOV-2000/ 99US-0248071.
PR 17-NOV-2000/ 99US-0248289.
PR 18-NOV-2000/ 99US-0248507.
PR 19-NOV-2000/ 99US-0248725.
PR 20
```


XX AAH97692;
 AC 25-SEP-2001 (first entry)
 XX Peppermint plant oil gland expressed cDNA 48.
 XX Peppermint; plant oil gland cell; terpenoid essential oil; resin;
 XX Genetic mapping; antisense suppression; recombinant expression; ss.
 XX Mencha x piperita.
 CG W200153319-A1.
 XX 26-JUL-2001.
 XX 19-JUN-2001; 2001WO-US02567.
 XX 20-JUN-2000, 2000US-0177264.
 XX (CROST/) CHOTRAU R B.
 XX (LANG/) LANGER B M.
 XX (WILD/) WILDUNG R R.
 XX Croteau RB, Lange BM, Wildung MR;
 XX WPI, 2001-488706/53.
 XX New nucleic acid molecules corresponding to mRNA molecules expressed in
 XX peppermint oil glands for enhancing expression of plant oil gland cell
 XX proteins - Page 95; 251pp; English.
 XX Claim 1: The invention relates to nucleic acid molecules (AAH9745-AAH98116) that
 XX code for all or part of the nucleic acid molecules that are naturally
 XX gland cells, especially peppermint and plant oil glands that produce
 XX terpenoid essential oils and resins. The nucleic acids are useful for
 XX genetically mapping a plant genome for genes expressed in plant oil
 XX enhance their expression (for example by genetically transforming a
 XX plant cell with a replicable expression vector that expresses one or more
 XX proteins naturally expressed in plant oil gland cells). The nucleic acids
 XX required for terpenoid recombinant expression of plant oil gland proteins
 XX and/or yeast cells.
 XX Sequence 645 BP; 194 A; 129 C; 132 G; 189 T; 1 other;
 XX Query Match 2.7%; Score 59.2; DB 22; Length 645;
 XX Best Local Similarity 54.1%; Pred. No. 8.3e-06;
 XX Matches 118; Conservative 1; Mismatches 99; Indels 0; Gaps 0;
 QY 1758 CCAACACGATGATCATCTTCGACAGATTTTCTGATGATATGATCTATCTATGCTCA 1817
 DB 210 CAAATCGAGAGCTTATATATGAGGATCTTTTCTGACACGGGTATGACATGCGCA 269
 QY 1818 TTATCCAGCTGACAGCTTCTGGAGAGCTGCTGATGACAGCTTCCTGATGCGGAT 1877
 DB 270 TATACATGATGCTGACAGCTGCTGAGTATGATGCTGATGATGATGATGATGATGAT 329
 QY 1878 CAAATGATGATGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1937
 DB 330 GAGATCTGCTGCTGCTGATGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCT 329
 QY 1998 GGGCT 1975
 DB 390 GCTACAGATGATGCTCTGGAGGCTGATGAGGAGCTGATGAGGAGCTGATGAGGAGCT 427
 XX FIGURE 14
 XX ABL72070
 ID ABL72070 standard; cDNA; 276 BP.

XX ABL72070;
 AC 14-MAY-2002 (first entry)
 XX Corn tassal-derived polynucleotide (cdps) SEQ ID NO:1444.
 XX Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPs;
 XX environmental adaptability; quality; yield; molecular marker;
 XX multigene trait; plant breeding; corn tassal; gene; ss.
 XX Zea mays.
 XX US2001051335-A1.
 XX 13-DEC-2001.
 XX 16-APR-1999; 99US-0294093.
 XX 21-APR-1998; 98US-082567P.
 XX (LANG/) LANGUDI R V.
 XX (TOL/) ITO L Y.
 XX (SHER/) SHERMAN B K.
 XX Laigudi RV, Ito LY, Sherman BK;
 XX NPT; 2002-463647/21.
 XX Novel purified corn tassal-derived polynucleotide useful for
 XX determining altered gene expression, to recover regulatory elements and
 XX to follow inheritance of desirable characteristics through hybrid
 XX breeding programs -
 XX Claim 1: SEQ ID 1444; 201pp; English.
 XX The present sequence describes a purified corn tassal-derived
 XX polynucleotide sequence (cdps) comprising a nucleic acid sequence
 XX encode corn tassal-derived polypeptides (CDPs). The cdps sequences (1)
 XX can be used for determining altered gene expression, to recover
 XX regulatory elements and to follow inheritance of desirable
 XX in the tassal through alteration of desired characteristics associated
 XX with growth and development, disease resistance, environmental
 XX adaptability, quality and yield, and as molecular markers for studying
 XX inheritance of multigene traits in a plant breeding program. (1) can be
 XX transcript in sage, to clone regulatory elements for use in transformation
 XX vectors, to express a polypeptide, to identify, isolate or extend
 XX identical or related corn tassal nucleic acid sequences from DNA libraries,
 XX as query sequences to determine homology of known sequences, as probe
 XX for use in Southern or Northern hybridization, and to identify the
 XX presence of and/or to determine the degree of similarity between two
 XX (or more) nucleic acid sequences.
 XX Sequence 276 BP; 73 A; 54 C; 79 G; 7 T; 0 other;
 XX Query Match 2.7%; Score 58.6; DB 24; Length 276;
 XX Best Local Similarity 5.0%; Pred. No. 0.0e-00;
 XX Matches 126; Conservative 0; Mismatches 94; Indels 1; Gaps 1;
 QY 1748 TGCACACACCAACAGATATGATCTTCGAAACATTTTCTATGATGATGACTT 1807
 DB 53 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 112
 QY 1808 CATCATGCTTACACGTGGAGAGCTTTTGGAAAGTCTTGATGACGTTTCTCGT 1867
 DB 113 CACTCTGCAATTAATCATGTGTGCTCCATGTAGAGAGAGTGTGTTCACGCTTACCGG 172
 QY 1868 TTATGGGATCNAAGCATTAGCGTTGTGATGCTCCAGTCTTCCTTCCCTCAACCAACA 1927

/ PRIOR APPLICATION NUMBER: A60/2001
 / PRIOR FILING DATE: 2001-01-16
 / PRIOR APPLICATION NUMBER: A523/2001
 / PRIOR FILING DATE: 2001-04-03
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: Patent In Ver. 2.1
 / SEQ ID NO 4
 / LENGTH: 68
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of the artificial sequence: Synthetic oligonucleotide
 US-10-046-232-4

Query Match 3.1%; Score 68; DB 15; Length 68;
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 CTATTGTGGTGCATCTCTGTTCTTCCTTCATCTGATTCAGAGGTTCATCTGGTTC 99
 DB 1 CTATTGTGGTGCATCTCTGTTCTTCCTTCATCTGATTCAGAGGTTCATCTGGTTC 60
 QY 100 ATATCTC 107
 DB 61 ATATCTC 68

RESULT 6
 US-09-770-961-453
 / Sequence 453, Application US/09770961
 / Best Local Similarity 100.0%; Pred. No. 0.11659A1
 / GENERAL INFORMATION: US/09770961
 / APPLICANT: Gorlach, Jörn
 / APPLICANT: An, Yong-Qiang
 / APPLICANT: Hamilton, Carol M.
 / APPLICANT: Raine, Tracy M.
 / APPLICANT: Yu, Yang
 / APPLICANT: Rameika, G.
 / APPLICANT: Mathew, Abraham V.
 / APPLICANT: Ledford, Brooke L.
 / APPLICANT: Woessner, Jeffrey P.
 / APPLICANT: Williams, William David
 / APPLICANT: Garcia, Cayla A.
 / APPLICANT: Kricker, Maja
 / APPLICANT: Slader, Ted
 / APPLICANT: Kivits, Keith R.
 / APPLICANT: Alvi, Michael
 / APPLICANT: Hoffman, Neil
 / APPLICANT: Durban, Patrick
 / TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 / FILE REFERENCE: 2001-188241/C/01553
 / CURRENT APPLICATION NUMBER: US/09/770,961
 / CURRENT FILING DATE: 2001-01-26
 / PRIOR FILING DATE: 2001-01-26
 / PRIOR APPLICATION NUMBER: 60/178,466
 / NUMBER OF SEQ ID NOS: 999
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 453
 / LENGTH: 439
 / TYPE: DNA
 / ORGANISM: Arabidopsis thaliana
 US-09-770-961-453

Query Match 3.1%; Score 66.6; DB 11; Length 499;
 Best Local Similarity 55.4%; Pred. No. 6.5e-07;
 Matches 129; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
 QY 1180 CTGCGGTGACGAGCACTTATCTTATCTGCGGACATGAGACGCTGCTCTTCA 1239
 DB 137 GAAGCGCCTTGATGAGATCATCTATGCGGACCACTAGGAGCTGACCTACTT 196

QY 1240 CTACTTATGTCGGTGGACAGGCTTACCTATCTCTCAACATCAGAGTTGTTGAC 1299
 DB 197 ATGCTATAGTGGTGTGGCCCATCCATGGCTCATATACAGGCCAAATCATCAGGTGATG 256
 QY 1300 CGAATCTCTTATGTTGGCAGCTTTGTGGATGATGATCACTCTGATATATTAATTTG 1359
 DB 257 GACCACTTATCTGGGTGAGGCACTGTATGACACCTTATGATGCGGTGGTGTCTCT 316
 QY 1360 CCCCACAAATCAATGATGAGCGCTCTGCTGACCTTACGAGCTTAGAGATGA 1412
 DB 317 TCTCAGTCCCGTGTGAGGCTCTCACTCATATGAGGTTGTGGGATACCGGGGA 369

RESULT 7
 US-10-046-232-9/c
 / Sequence 9, Application US/10046232
 / Best Local Similarity 100.0%; Pred. No. 0.00119093A1
 / GENERAL INFORMATION: US/00119093A1
 / APPLICANT: Helmut SCHWAB
 / APPLICANT: Anton GLIEDER
 / APPLICANT: Christoph KEATY
 / APPLICANT: Peter POCHLAUER
 / APPLICANT: Wolfgang SKRANC
 / APPLICANT: Herbert MAYHOFFER
 / APPLICANT: Rainer WITTMANN
 / APPLICANT: Rudolf NEUHOFER
 / APPLICANT: Rodolfo BONA
 / TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile
 / TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitrile
 / FILE REFERENCE: 2001-188241/C/01553
 / CURRENT APPLICATION NUMBER: US/10/046,232
 / CURRENT FILING DATE: 2002-10-31
 / PRIOR FILING DATE: 2001-01-16/2001
 / PRIOR APPLICATION NUMBER: A523/2001
 / PRIOR FILING DATE: 2001-04-03
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: Patent In Ver. 2.1
 / SEQ ID NO 9
 / LENGTH: 73
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of the artificial sequence: Synthetic oligonucleotide
 US-10-046-232-9

Query Match 3.0%; Score 65; DB 15; Length 73;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2097 CTGCAAGAGGCTCATCGGTGGAGCTTATCTATATATTCAGAGTCCATGAGAG 2156
 DB 73 CTGCAAGAGGCTCATCGGTGGAGCTTATCTATATATTCAGAGTCCATGAGAG 14
 QY 2157 ATTCG 2161
 DB 13 ATTCG 9

RESULT 8
 US-09-770-445-404/c
 / Sequence 404, Application US/09770445
 / Patent No. US200202381A1
 / GENERAL INFORMATION: US/09770445
 / APPLICANT: Kowalsch, Jörn
 / APPLICANT: An, Yong-Qiang
 / APPLICANT: Hamilton, Carol M.
 / APPLICANT: Price, Jennifer L.
 / APPLICANT: Mathew, Abraham V.
 / APPLICANT: Yu, Yang

; Sequence 909, Application US/09770444
 ; Patent No. US20020023280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorkach, Jörn

```

/ APPLICANT: An, Yong-Qiang
/ APPLICANT: Am, Yong-Qiang
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Yu, Yang
/ APPLICANT: Rameaka, Joshua G.
/ APPLICANT: Page, Amy
/ APPLICANT: Rameaka, Joshua G.
/ APPLICANT: Leedford, Jeffrey P.
/ APPLICANT: Leedford, Jeffrey P.
/ APPLICANT: Haas, William David
/ APPLICANT: Garcia, Carlos A.
/ APPLICANT: Slader, Ted A.
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Richman, Patrick
/ APPLICANT: Richman, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
/ TITLE OF INVENTION: thaliana
/ CURRENT REFERENCE: 2027 (GARA-01698V)
/ CURRENT FILING DATE: 2000-01-26
/ PRIOR APPLICATION NUMBER: 60/178,502
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ NOS: 999
/ SOFTWARE: PARSSEQ for Windows Version 4.0
/ SEQ ID NO 909
/ LENGTH: 441
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-05-770-444-909

Query Match      2.54; Score 54.6; DB 9; Length 441;
Seq Similarity 56.44; Pred. No. 0.0086;
Matches 102; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1795 GATATGTAGCTTATCTAGCTGATACACGAGTGGAACTTGTGGAAAGTCTGAT 1854
Db 441 GATTCCTGTGACATTTATTCATTCCTGGAGTGTGTTGATGGAAGAGTCTGAC 382

Qy 1855 GAGATCTTCGGTGTATGGGATCAAGGATTAACGGTGTATGATGCTTCACATTCCT 1914
Db 381 AAGATCAACAAAGCATATGGGTTGTTGTGATGATCTGATGATGCTGCTGCTGCT 322

Qy 1915 TAGCAACAAAGCATATGGGTTGTTGTGATGATCTGATGATGCTGCTGCTGCT 1974
Db 321 AGTCTTCGGGAGCATATTCATCCAGCCACATCATATCTGAGCATATATGAGGCG 262

Qy 1975 A 1975
Db 261 A 261

RESULT 12
US-05-878-574-207
/ Patent No. US20020110548A1
/ APPLICATION: Application US/09878574
/ GENERAL INFORMATION:
/ APPLICANT: Byrum, Joseph R.
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: La Rosa, Thomas J.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules associated with
/ FILE REFERENCE: 38-21(15401)B
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,435
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 2850
/ LENGTH: 267
/ TYPE: DNA

```

```

/ ORGANISM: Glycine max
/ OTHER INFORMATION: Clone ID: L1B3028-053-Q1-B1-G4
US-09-878-574-207

Query Match      2.48; Score 51.2; DB 10; Length 267;
Seq Local Similarity 59.71; Pred. No. 0.005; Mismatches 56; Indels 0; Gaps 0;
Matches 86; Conservative 0;

Qy 1825 GCGGAGAGCTTGTGGGAAAGTCTGTATGACGATCTTCGCTGTATGGGATCAACA 1884
Db 1 GCGAGGTGGCAATCTGTGTAGGTGTCATCATATATATGAGTATATGTGTGACT 60

Qy 1885 TTAGCTGTGTATGATCTCTCTCCCTTATGACCAACAAAGCCGCTCTGAGGCTTC 1944
Db 61 TTGAGGTGAATGATGATGATCTCTCTCCCTTATGACCAACAAAGCCGCTCTGAGTACT 120

Qy 1945 TATCTGTATGTAGGAGATATGTG 1968
Db 121 GTATGATCTCTGAGGATATG 144

RESULT 13
US-10-042-232-3
/ Sequence 3, Application US/10046232
/ Publication No. US20030119099A1
/ GENERAL INFORMATION:
/ APPLICANT: Helmut Schrae
/ APPLICANT: Helmut Schrae
/ APPLICANT: Christoph Keatky
/ APPLICANT: Ingrid Dreveny
/ APPLICANT: Peter Pochlaue
/ APPLICANT: Helmut Schrae
/ APPLICANT: Herbert Mayhoefer
/ APPLICANT: Irma Wirth
/ APPLICANT: Rudolf Neuhöfer
/ APPLICANT: Rudolf Neuhöfer
/ TITLE OF INVENTION: Non genes containing a DNA sequence coding for a hydroxymethyl
/ TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxymethyl
/ TITLE OF INVENTION: thereof
/ CURRENT REFERENCE: 100.18876/US/01559
/ CURRENT FILING DATE: 2002-10-31
/ CURRENT APPLICATION NUMBER: US/0946,232
/ PRIOR APPLICATION NUMBER: A60/2001
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR FILING DATE: 2001-04-03
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 108
/ LENGTH: 64
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURES: Description of the artificial sequence: Synthetic oligonucleotide
US-10-046-232-3

Query Match      2.31; Score 49; DB 15; Length 64;
Seq Similarity 100.04; Pred. No. 0.008; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 0;

Qy 13 ATGAGAAATACACATGATGATATCTATTTGTCCTCTCTTG 61
Db 16 ATGAGAAATACACATGATGATATCTATTTGTCCTCTCTTG 64

RESULT 14
US-10-042-232-8/c
/ Sequence 8, Application US/10046232
/ Publication No. US20030119099A1
/ GENERAL INFORMATION:
/ APPLICANT: Helmut Schrae
/ APPLICANT: Helmut Schrae
/ APPLICANT: Christoph Keatky

```


GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 15:05:47, Search time 130 seconds
(without alignments)
7340.391 Million call updates/sec

Title: US-10-046-232-19

Perfect score: 2162

Sequence: 1 ggcattccatagagagaa.....agtcctatgagatctggc 2162

Scoring table: IDENTITY NUC

Gapop 10.0, Deapex 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 113956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 0%

Listing first 45 summaries

Database: 1 Issued Patents MA.*2/ins/EA COMB.seq*

2 /csm2_5/prodata/2/ins/EA COMB.seq*

3 /csm2_5/prodata/2/ins/EA COMB.seq*

4 /csm2_5/prodata/2/ins/EA COMB.seq*

5 /csm2_5/prodata/2/ins/EA COMB.seq*

6 /csm2_5/prodata/2/ins/EA COMB.seq*

7 /csm2_5/prodata/2/ins/EA COMB.seq*

8 /csm2_5/prodata/2/ins/EA COMB.seq*

9 /csm2_5/prodata/2/ins/EA COMB.seq*

10 /csm2_5/prodata/2/ins/EA COMB.seq*

11 /csm2_5/prodata/2/ins/EA COMB.seq*

12 /csm2_5/prodata/2/ins/EA COMB.seq*

13 /csm2_5/prodata/2/ins/EA COMB.seq*

14 /csm2_5/prodata/2/ins/EA COMB.seq*

15 /csm2_5/prodata/2/ins/EA COMB.seq*

16 /csm2_5/prodata/2/ins/EA COMB.seq*

17 /csm2_5/prodata/2/ins/EA COMB.seq*

18 /csm2_5/prodata/2/ins/EA COMB.seq*

19 /csm2_5/prodata/2/ins/EA COMB.seq*

20 /csm2_5/prodata/2/ins/EA COMB.seq*

21 /csm2_5/prodata/2/ins/EA COMB.seq*

22 /csm2_5/prodata/2/ins/EA COMB.seq*

23 /csm2_5/prodata/2/ins/EA COMB.seq*

24 /csm2_5/prodata/2/ins/EA COMB.seq*

25 /csm2_5/prodata/2/ins/EA COMB.seq*

26 /csm2_5/prodata/2/ins/EA COMB.seq*

27 /csm2_5/prodata/2/ins/EA COMB.seq*

28 /csm2_5/prodata/2/ins/EA COMB.seq*

29 /csm2_5/prodata/2/ins/EA COMB.seq*

30 /csm2_5/prodata/2/ins/EA COMB.seq*

31 /csm2_5/prodata/2/ins/EA COMB.seq*

32 /csm2_5/prodata/2/ins/EA COMB.seq*

33 /csm2_5/prodata/2/ins/EA COMB.seq*

34 /csm2_5/prodata/2/ins/EA COMB.seq*

35 /csm2_5/prodata/2/ins/EA COMB.seq*

36 /csm2_5/prodata/2/ins/EA COMB.seq*

37 /csm2_5/prodata/2/ins/EA COMB.seq*

38 /csm2_5/prodata/2/ins/EA COMB.seq*

39 /csm2_5/prodata/2/ins/EA COMB.seq*

40 /csm2_5/prodata/2/ins/EA COMB.seq*

41 /csm2_5/prodata/2/ins/EA COMB.seq*

42 /csm2_5/prodata/2/ins/EA COMB.seq*

43 /csm2_5/prodata/2/ins/EA COMB.seq*

44 /csm2_5/prodata/2/ins/EA COMB.seq*

45 /csm2_5/prodata/2/ins/EA COMB.seq*

46 /csm2_5/prodata/2/ins/EA COMB.seq*

47 /csm2_5/prodata/2/ins/EA COMB.seq*

48 /csm2_5/prodata/2/ins/EA COMB.seq*

49 /csm2_5/prodata/2/ins/EA COMB.seq*

50 /csm2_5/prodata/2/ins/EA COMB.seq*

28 35 1.6 294 4 US-08-134-001C-2110
Sequence 1, Appl
30 34.8 1.6 2098 4 US-08-749-391-1
Sequence 1, Appl
31 34.6 1.6 2058 3 US-09-390-200-1
Sequence 534, Appl
32 34.6 1.6 4854 4 US-08-841-527-178
Sequence 178, Appl
33 34.4 1.6 3509 4 US-09-255-829-178
Sequence 19, Appl
34 34.4 1.6 4037 1 US-08-844-085-1
Sequence 1, Appl
35 34.2 1.6 4259 3 US-09-078-557-2
Sequence 2, Appl
36 34.2 1.6 4344 4 US-09-601-136-165
Sequence 165, Appl
37 34.2 1.6 1664976 4 US-08-916-421B-1
Sequence 1, Appl
38 34.2 1.6 390 1 US-08-844-085-3
Sequence 1, Appl
39 34.2 1.6 747 5 PCT-US94-06430-1
Sequence 1, Appl
40 33.8 1.6 879 3 US-08-591-468-5
Sequence 5, Appl
41 33.8 1.6 829 5 PCT-US94-06430-5
Sequence 5, Appl
42 33.8 1.6 1277 3 US-09-347-803-3
Sequence 3, Appl
43 33.8 1.6 1277 3 US-09-347-803-3
Sequence 3, Appl
44 33.8 1.6 1277 3 US-09-347-803-3
Sequence 3, Appl
45 33.8 1.6 1277 3 US-09-347-803-3
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
PCT-US94-06430-1
GENERAL INFORMATION:
APPLICANT: DORNER, F.
INVENTOR: CHEILINER, F.
TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/995.313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-Aug-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29 768
REFERENCE/SOCKET NUMBER: 30472/114 INO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/683-4139
TELEFAX: 703/683-4139
TELEX: 699149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2162
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INSTRUMENT: ABI PRISM 310
CLONE: JVTGPF-F16
US-08-232-463-14

Query Match 2.7% Score 58.8; DB 1; Length 7218;

Result No.	Score	Query Match	Length	DB ID	Description
1	58.8	2.7	7218	US-08-232-463-14	Sequence 1, Appl
2	45	2.1	1863	US-09-443-087-1	Sequence 1, Appl
3	45	2.1	1863	US-09-443-087-1	Sequence 1, Appl
4	45	2.1	1863	US-09-687-298-1	Sequence 1, Appl
5	41.2	1.9	1497	US-09-230-132-94	Sequence 94, Appl
6	40.0	1.9	6527	US-09-432-308A-3	Sequence 3, Appl
7	39.8	1.8	1737	US-09-328-352-1553	Sequence 1553, Ap
8	39.8	1.8	1737	US-09-155-078-1	Sequence 1, Appl
9	38.4	1.8	3431	US-09-155-078-1	Sequence 1, Appl
10	36.8	1.7	180131	US-09-537-863-1	Sequence 848, Appl
11	36.8	1.7	180131	US-09-537-863-1	Sequence 848, Appl
12	36.8	1.7	180131	US-09-541-990A-1	Sequence 1, Appl
13	36.2	1.7	168575	US-09-426-280-1	Sequence 1, Appl
14	36	1.7	3194	US-08-601-139-17	Sequence 17, Appl
15	35	1.7	10659	US-08-961-527-57	Sequence 57, Appl
16	35.8	1.7	10659	US-08-961-527-57	Sequence 57, Appl
17	35.8	1.7	1664976	US-08-916-421B-1	Sequence 1, Appl
18	35.6	1.6	2277	US-08-676-967-2	Sequence 2, Appl
19	35.6	1.6	2277	US-08-676-967-2	Sequence 2, Appl
20	35.6	1.6	2277	US-09-098-407-2	Sequence 2, Appl
21	35.4	1.6	795	US-09-134-001C-943	Sequence 943, Appl
22	35.4	1.6	19718	US-08-961-527-99	Sequence 99, Appl
23	35.2	1.6	3212	US-08-961-527-99	Sequence 99, Appl
24	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
25	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
26	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
27	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
28	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
29	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
30	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
31	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
32	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
33	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
34	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
35	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
36	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
37	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
38	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
39	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
40	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
41	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
42	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
43	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
44	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
45	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
46	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
47	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
48	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
49	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
50	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
51	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
52	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
53	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
54	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
55	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
56	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
57	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
58	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
59	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
60	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
61	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
62	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
63	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
64	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
65	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
66	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
67	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
68	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
69	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
70	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
71	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
72	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
73	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
74	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
75	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
76	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
77	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
78	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
79	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
80	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
81	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
82	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
83	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
84	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
85	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
86	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
87	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
88	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
89	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
90	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
91	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
92	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
93	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
94	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
95	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
96	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
97	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
98	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
99	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl
100	35.2	1.6	3212	US-08-961-527-99	Sequence 1, Appl

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the data source distribution.

SUMMARIES

Best Local Similarity 3.24; Pred. No. 1.1e-06;
Matches 12; Conservative 216; Mismatches 140; Indels 0; Gaps 0;

QY 1203 TGATATGCGGAGCATCGAGACCGCTCAGCTCTACTACTAGTGGCGTGGACAGA 1262
DB 1044 TCGAGTGTGAGGAGCTGCGATYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 1103
QY 1263 GCTCTACTATCTCTCTACATCAGAGTGTGTGCGGACATCTATGTGGCGGTT 1322
DB 1104 YVY 1163
QY 1323 TGTGTAGCAATCTGTAATCTTANTATTTTGGCCCAATCCAATGAGCTTC 1383
DB 1164 YVY 1223
QY 1283 TGTGTACATCTTGTAGGCAATATATCAAGTCTTCTCTCAAGCTGCC 1442
DB 1224 YVY 1283
QY 1443 ATTTCCTCAGCCTTTAGTCTTTCTTCTCAAGCTCTACCGCTCCCAATGCGAC 1502
DB 1284 YVY 1343
QY 1503 TTGTGTCATATGTAGCAAGTGTGAGACGATGTCTGTGCTGCTGCAAGTAA 1562
DB 1344 YVY 1403
QY 1563 TTCAGTACT 1572
DB 1404 YVY 1413

RESULT 2
US-09-199-229-1
; Sequence 1, Application US/09199229
; Title of Invention: Activity And Nucleic Acids Encoding Same
; General Information:
; Applicant: Yaver, Debbie S.
; Applicant: Michael W. Rey
; Applicant: Randy M. Berka
; Title of Invention: Polypeptides Having Choline Oxidase
; Title of Invention: Activity And Nucleic Acids Encoding Same
; File Reference: 5735.000-US
; Current Filing Date: 1998-11-24
; Number of Seq ID NOS: 2
; Software: FastSeq for Windows Version 3.0
; Seq ID No: 1
; Seq ID No: 2
; Type: DNA
; Organism: Fusarium venenatum
US-09-199-229-1

Query Match 2.18; Score 45; DB 3; Length 1863;
Best Local Similarity 55.41; Pred. No. 0.0055;
Matches 87; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1195 GAGCTATTTGTATGTGAGGAGCATCGAGACGCTCAGCTCTACTACTAGTGGCTT 1254
DB 820 GAGCATTTCTTGTGCGCGCGCTGCTGATGACAGAGCTCTCTCCACTCTGGATT 879
QY 1255 GCGACAGCTTACTACTATCTCTCTCAAGTCAAGTGTGTGCGGAGCTCTATGT 1314
DB 880 GCGCCCAAGGCTCAGCTCTCTCAAGTCTCTCAAGTCCCGGTGTGCAAGACATCC 939
QY 1315 GCGAGTTTGTATGAATCTCTGATTTCTA 1351
DB 940 GCGCAAACTCTTGATGATCCCGGAGACATATCA 976

RESULT 3
US-09-443-087-1
; Sequence 1, Application US/0943087

Patent No. 514664
GENERAL INFORMATION:
; Applicant: Debbie Yaver
; Applicant: Randy M. Berka
; Applicant: Michael W. Rey
; Title of Invention: Polypeptides Having Choline Oxidase
; Title of Invention: Activity And Nucleic Acids Encoding Same
; File Reference: 5735.200-US
; Current Application Number: US/09/443,087
; Current Filing Date: 1998-11-24
; Earlier Application Number: US/09/199,229
; Earlier Filing Date: 1998-11-24
; Number of Seq ID NOS: 2
; Software: FastSeq for Windows Version 3.0
; Seq ID No: 1
; Seq ID No: 2
; Type: DNA
; Organism: Fusarium venenatum
US-09-443-087-1

Query Match 2.18; Score 45; DB 3; Length 1863;
Best Local Similarity 55.41; Pred. No. 0.0055;
Matches 87; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1195 GAGCTATTTGTATGTGAGGAGCATCGAGACGCTCAGCTCTACTACTAGTGGCTT 1254
DB 820 GAGCATTTCTTGTGCGCGCGCTGCTGATGACAGAGCTCTCTCCACTCTGGATT 879
QY 1255 GCGACAGCTTACTACTATCTCTCTCAAGTCAAGTGTGTGCGGAGCTCTATGT 1314
DB 880 GCGCCCAAGGCTCAGCTCTCTCAAGTCTCTCAAGTCCCGGTGTGCAAGACATCC 939
QY 1315 GCGAGTTTGTATGAATCTCTGATTTCTA 1351
DB 940 GCGCAAACTCTTGATGATCCCGGAGACATATCA 976

RESULT 4
US-09-687-298-1
; Sequence 1, Application US/09687298
; Title of Invention: Activity And Nucleic Acids Encoding Same
; General Information:
; Applicant: Debbie Yaver
; Applicant: Randy M. Berka
; Applicant: Michael W. Rey
; Title of Invention: Polypeptides Having Choline Oxidase
; Title of Invention: Activity And Nucleic Acids Encoding Same
; File Reference: 5735.200-US
; Current Application Number: US/09/687,298
; Current Filing Date: 1998-11-24
; Prior Application Number: US/09/443,087
; Prior Filing Date: 1999-11-18
; Number of Seq ID NOS: 2
; Software: FastSeq for Windows Version 3.0
; Seq ID No: 1
; Seq ID No: 2
; Type: DNA
; Organism: Fusarium venenatum
US-09-687-298-1

Query Match 2.18; Score 45; DB 4; Length 1863;
Best Local Similarity 55.41; Pred. No. 0.0055;
Matches 87; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1195 GAGCTATTTGTATGTGAGGAGCATCGAGACGCTCAGCTCTACTACTAGTGGCTT 1254
DB 820 GAGCATTTCTTGTGCGCGCGCTGCTGATGACAGAGCTCTCTCCACTCTGGATT 879
QY 1255 GCGACAGCTTACTACTATCTCTCTCAAGTCAAGTGTGTGCGGAGCTCTATGT 1314
DB 880 GCGCCCAAGGCTCAGCTCTCTCAAGTCTCTCAAGTCCCGGTGTGCAAGACATCC 939
QY 1315 GCGAGTTTGTATGAATCTCTGATTTCTA 1351

Db 940 GCGGAAACCTCTTGATATCCGCGAGACCATATCA 976
 RESULT 5
 US-09-220-132-94/c Application US/09220132
 Patent No. 6506607
 GENERAL INFORMATION:
 APPLICANT: Sylvan, Andrew W.
 TITLE OF INVENTION: ORGANOGENIC CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
 TITLE OF INVENTION: ORGANOGENIC CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 07334-074001
 CURRENT APPLICATION NUMBER: US/09/220,132
 PRIORITY DATE: 1998-12-23
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: US 60/068,821
 PRIOR FILING DATE: 1997-12-24
 SOFTWARE: PMSREQ for Windows Version 4.0
 SEQ ID NO 94
 LENGTH: 1497
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION (1) : (1497)
 COMPOSITION: n = A,T,C or G
 US-09-220-132-94

Query Match 1.9%; Score 41.2; DB 4; Length 1497;
 Best Local Similarity 27.6%; Pred. No. 0.062;
 Matches 61; Conservative 65; Mismatches 103; Indels 0; Gaps 0;
 Qy 130 TCGATTCATTATACGACCAAAATCTGTAGATTATATTAAGAAACTGACACAGTAG 189
 Db 589 TATATATCTTTTAAATATATTTTGGGGCATGATAGTATGAGTATAC 530
 Qy 120 TCGAGAACACAGCTATTATAGATGATGATGAAAAAATCTTCTTCACATATA 249
 Db 529 ATCCGAGATATTTGGGATATTTAAATATATACAAATACAAATTTTCMCAR 470
 Qy 250 TTTTGACAGATTATGACTGAACTTTGTGTAGAACCAACCATCAAGCTCGAAG 309
 Db 469 WHYCCWATTTWSSWMTCTKSYTWKAWSCCCGCGGCTCKTMRGCTGEMAY 410
 Qy 310 ATCATATGATCTACTGATGCTGCGTGAGAGACTCAGGCTGCTCATGCGCA 361
 Db 409 TGAATTAATTAATTTKATTTWAWKCKSYGGRAMKSTTTTTCNKYTCM 358

RESULT 6
 US-08-232-463-14/c Application US/08232463
 Patent No. 6523984-3/c
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEFFLINGER, F.
 TITLE OF INVENTION: RECOMBINANT POWLOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESS: Foley & Lardner
 STREET: 3000 Reginald Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 SEQ ID NO 99
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 CLASSIFICATION: 435
 PRIOR APPLICATION NUMBER: US/07/935,313
 FILING DATE: 26-AUG-1991
 APPLICATION NUMBER: EP 91 114 300.6
 ATTORNEY/AGENT INFORMATION:
 NAME: BENJ, Stephen A.
 REFERENCE/DOCKET NUMBER: 39472/114 INWU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEFAX: (904) 683-4109
 INFORMATION FOR SEQ ID NO: 14:
 LENGTH: 7218 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: PT99P-Fls
 US-08-232-463-14
 Query Match 1.9%; Score 40.8; DB 1; Length 7218;
 Best Local Similarity 11.4%; Pred. No. 0.18;
 Matches 57; Conservative 207; Mismatches 234; Indels 0; Gaps 0;
 Qy 134 TATTCTATTACAGCAAAATGTGATTTATTAAGAACTGACACAGATGCA 193
 Db 1470 TATCCAGTGTATAGATAGAGATTGTGACRERERERERERERERERER 1411
 Qy 194 AGAACAGCACTAATTAGATGCAATGTGAAAAAATCTTCATCTTCATATTT 253
 Db 1410 ER 1351
 Qy 284 GCAGATTATTAAGTCTGAGTTGTGTACAGCCATGATACAGCTCGAGATCA 313
 Db 1350 ER 1291
 Qy 314 TATGATCATATTAATGTGTGGAGACATCGAGGTCTCATGCGAGACTTTTCA 373
 Db 1290 ER 1231
 Qy 374 GAARATATACAGCTCTCTCTGAGAGAGGCACTTTCTGATGATACCGACAG 433
 Db 1230 RRRRRRRERERERERERERERERERERERERERERERERERERER 1171
 Qy 434 TTGATCGATGGTGTGATATATCTGACACAGATGAGAAAGACCACTT 493
 Db 1170 ER 1111
 Qy 494 GAAGGTGTGTCGAGAGCGCATGATGTGCGAGCAGGATCTCTGCGACG 583
 Db 1110 RRRRRRRERERERERERERERERERERERERERERERERERERER 1051
 Qy 584 ACCTATATCATCGAGGTCTGCGGACGCACTAATCTTATGATGATGACAGA 613
 Db 1050 ACTGCGACGACGCGATTTATGCTGAGCTATGCGACGAGGAAATTTT 991
 Qy 614 ATGATGAGGACTCGAT 631
 Db 990 AATGATGCGGCTCGAT 973
 RESULT 7
 US-08-232-3084-3/c Application US/094923084
 Patent No. 6571430

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

1

70 *Journal of Management Inquiry*


```

Qy 117 TAATTTTCATCTTCAGTATTCATTACACCAAAATGCTAGATTATTAATTAAGAAA 176
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 826 TAATCTTAATATCTTTACTTACATGATTTTCGCTATTAATTAATTTAGTAAAGAA 885
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 177 CTGACACAGTAGTCAAGAAACAGCTAAATTTAGATGATGCTTTGAAAAAATCTTCAT 236
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 886 ATTCACAGATTAATTAATTAACAGAGCGCTTTATTTGTTCTTAATTAATTAATTA 945
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 237 CTCTTCACATATATTTTSCAGATTTTACCTACTTGAAGTTTGTG 280
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 946 ACTCTCAAGAGCTTTAGAAAAATTTTATTTTCTTTATTTTGG 989
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 15
US-08-894-731-1
/ Subject 1 Application US/08894731
/ Patent No. 6084089
/ GENERAL INFORMATION:
/ APPLICANT: MINO, Toshiki
/ INVENTOR: MINO, Toshiki
/ APPLICANT: HIYOSHI, Toru
/ APPLICANT: KASAKA, Keisuke
/ TITLE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE
/ CURRENT APPLICATION NUMBER: US/08/894,731
/ NUMBER OF SEQ ID NOS: 8
/ SOURCE: Patent in Ver. 2.0
/ SEQ ID NO. 1
/ LENGTH: 3600
/ TYPE: DNA
/ ORGANISM: Solanum tuberosum
US-08-894-731-1

```

```

Query Match 1-74; Score 36; Ds 3; Length 3600;
/ Similarity: 51.34; Gaps: 0; Mismatches: 75; Indels 0; Gaps 0;
Matches 81; Conservative 0;
Qy 112 ONCTGTAATTTTCATCTTCAGTATTCATTACACCAAAATGCTAGATTATTAATTA 171
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1841 GATTTTAATTAATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1900
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 GAATCTGACACAGTAGTCAAGAAACAGCTAAATTTAGATGATGCTTTGAAAAAATCT 231
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1901 AAAAATTTAGTATTTGAAATGATGCTGCAATTTCAAACTGATGAGCATTT 1960
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 232 TTATCTCTTCATCTTCAGTATTCATTACACCAAAATGCTAGATTATTAATTA 267
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1961 TTAAATCTGAAAAATTTTAACAAATTTTCAA 1996
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: December 18, 2003, 17:29:01
Job time : 142 secs